

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:16:02 ; Search time 62.7613 Seconds  
(without alignments)  
1359.585 Million cell updates/sec

Title: PCT-US03-05147-3  
Perfect score: 1643  
Sequence: 1 METDTLLLVWVLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No.    | Score | %<br>Query<br>Match | Length | DB       | ID                 | Description |
|--------|--------|-------|---------------------|--------|----------|--------------------|-------------|
| 1      | 1643   | 100.0 | 302                 | 4      | AAB60699 | Aab60699 Mouse IgG |             |
| 2      | 1643   | 100.0 | 302                 | 4      | AAE00507 | Aae00507 Human BCM |             |
| 3      | 1488.5 | 90.6  | 283                 | 5      | AAE15488 | Aae15488 Human BCM |             |
| 4      | 1398.5 | 85.1  | 281                 | 5      | AAE15489 | Aae15489 Mouse BCM |             |
| 5      | 1379   | 83.9  | 334                 | 5      | AAO14133 | Aao14133 Protein o |             |
| 6      | 1376   | 83.7  | 366                 | 5      | AAO14132 | Aao14132 Protein o |             |
| 7      | 1361   | 82.8  | 320                 | 5      | AAE22245 | Aae22245 Murine Ig |             |
| 8      | 1361   | 82.8  | 320                 | 6      | ABR55865 | Abr55865 Human imm |             |
| 9      | 1271   | 77.4  | 332                 | 6      | AAE35228 | Aae35228 Human TAC |             |

|    |        |      |     |   |          |          |           |
|----|--------|------|-----|---|----------|----------|-----------|
| 10 | 1269   | 77.2 | 446 | 4 | AAE13055 | Aae13055 | ADAM-17di |
| 11 | 1268.5 | 77.2 | 633 | 3 | AAy84965 | Aay84965 | Amino aci |
| 12 | 1265.5 | 77.0 | 465 | 4 | AAE13053 | Aae13053 | ADAM-10di |
| 13 | 1264.5 | 77.0 | 404 | 5 | AAO14136 | Aao14136 | Protein o |
| 14 | 1263   | 76.9 | 348 | 6 | AAE35225 | Aae35225 | Human TAC |
| 15 | 1260   | 76.7 | 608 | 6 | ABJ37102 | Abj37102 | Concatame |
| 16 | 1259.5 | 76.7 | 397 | 5 | AAE15498 | Aae15498 | Human TAC |
| 17 | 1259   | 76.6 | 480 | 6 | AAO16239 | Aao16239 | B7-relate |
| 18 | 1259   | 76.6 | 480 | 6 | AAO16238 | Aao16238 | B7-relate |
| 19 | 1259   | 76.6 | 698 | 5 | AAU81012 | Aau81012 | B7-relate |
| 20 | 1259   | 76.6 | 698 | 6 | AAO16237 | Aao16237 | B7-relate |
| 21 | 1258   | 76.6 | 344 | 6 | AAE35224 | Aae35224 | Human TAC |
| 22 | 1257.5 | 76.5 | 376 | 2 | AAW60037 | Aaw60037 | Antigenic |
| 23 | 1256   | 76.4 | 422 | 4 | AAB66993 | Aab66993 | OPG-Fc. 4 |
| 24 | 1254   | 76.3 | 266 | 5 | ABB77128 | Abb77128 | Human Cri |
| 25 | 1254   | 76.3 | 266 | 5 | ABB77121 | Abb77121 | Human Cri |
| 26 | 1254   | 76.3 | 494 | 4 | AAE13051 | Aae13051 | ADAM-8dis |
| 27 | 1253.5 | 76.3 | 357 | 6 | AAE35226 | Aae35226 | Human TAC |
| 28 | 1252   | 76.2 | 266 | 5 | ABB77108 | Abb77108 | Human Cri |
| 29 | 1252   | 76.2 | 266 | 5 | ABB77115 | Abb77115 | Human Cri |
| 30 | 1252   | 76.2 | 444 | 6 | ABJ37098 | Abj37098 | Concatame |
| 31 | 1252   | 76.2 | 628 | 6 | ABJ37100 | Abj37100 | Concatame |
| 32 | 1251.5 | 76.2 | 523 | 4 | AAE13057 | Aae13057 | ADAM-21di |
| 33 | 1251   | 76.1 | 400 | 4 | AAB80901 | Aab80901 | Human OPG |
| 34 | 1251   | 76.1 | 400 | 4 | AAy72919 | Aay72919 | Human OPG |
| 35 | 1251   | 76.1 | 445 | 2 | AAy24153 | Aay24153 | Bovine LO |
| 36 | 1250.5 | 76.1 | 387 | 2 | AAR90920 | Aar90920 | IL4.Y124D |
| 37 | 1249   | 76.0 | 252 | 6 | ABJ38342 | Abj38342 | TALL-1 in |
| 38 | 1249   | 76.0 | 528 | 4 | AAE13061 | Aae13061 | ADAM-29di |
| 39 | 1248.5 | 76.0 | 503 | 6 | ABP72602 | Abp72602 | Human LP2 |
| 40 | 1248.5 | 76.0 | 535 | 2 | AAy17414 | Aay17414 | SVPH1-26  |
| 41 | 1248.5 | 76.0 | 535 | 4 | AAE13056 | Aae13056 | ADAM-20di |
| 42 | 1248   | 76.0 | 287 | 4 | AAB47590 | Aab47590 | Fusion pr |
| 43 | 1248   | 76.0 | 358 | 6 | ABP98040 | Abp98040 | Amino aci |
| 44 | 1247   | 75.9 | 380 | 5 | AAU97114 | Aau97114 | Human MK6 |
| 45 | 1246.5 | 75.9 | 717 | 6 | ABP72600 | Abp72600 | Human LP2 |

#### ALIGNMENTS

##### RESULT 1

AAB60699

ID AAB60699 standard; protein; 302 AA.

XX

AC AAB60699;

XX

DT 11-SEP-2003 (revised)

DT 22-MAY-2001 (first entry)

XX

DE Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.

XX

KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
immune-related disorder; B-cell growth inhibitor;

KW B-cell maturation inhibitor; immunoglobulin production inhibitor;

KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

KW renal disorder; immunosuppressive disorder; HIV infection;

KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
 KW lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Chimeric.  
 XX  
 PN WO200112812-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 16-AUG-2000; 2000WO-US022507.  
 XX  
 PR 17-AUG-1999; 99US-0149378P.  
 PR 11-FEB-2000; 2000US-0181684P.  
 PR 18-FEB-2000; 2000US-0183536P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA (APOT-) APOTECH R & D SA.  
 XX  
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
 PI Thompson J;  
 XX  
 DR WPI; 2001-202866/20.  
 DR N-PSDB; AAF59999.  
 XX  
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
 PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
 XX  
 PS Example 4; Fig 2; 59pp; English.  
 XX  
 CC The invention relates to the use of a BAFF receptor (BAFF-R, also known  
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
 CC agent, and also plays a role in the development of hypertension and  
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also  
 CC be used in the treatment of immunosuppressive disorders and HIV  
 CC infection, and in patients undergoing organ transplantation. The BAFF-R  
 CC proteins or BAFF-R specific antibodies may be used for treating,  
 CC suppressing or altering an immune response involving a signalling pathway  
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R  
 CC inhibits B-cell growth and maturation it is useful for treating diseases  
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,  
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly  
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding  
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,  
 CC autoimmune disorders and inherited B-cell-associated disorders. The  
 CC present sequence represents the BAFF-R fusion protein BAFF-R-Fc,  
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human

CC BAFF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 302 AA;

Query Match 100.0%; Score 1643; DB 4; Length 302;  
Best Local Similarity 100.0%; Pred. No. 1.4e-111;  
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METDTLLLWVLLLWVPGSTGDVMTLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTC 60  
|  
Db 1 METDTLLLWVLLLWVPGSTGDVMTLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTC 60  
  
Qy 61 QRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 120  
|  
Db 61 QRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 120  
  
Qy 121 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 180  
|  
Db 121 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 180  
  
Qy 181 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 240  
|  
Db 181 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 240  
  
Qy 241 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 300  
|  
Db 241 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 300  
  
Qy 301 GK 302  
||  
Db 301 GK 302

## RESULT 2

AAE00507

ID AAE00507 standard; protein; 302 AA.

XX

AC

AAE00507;

XX

DT

11-SEP-2003 (revised)

DT

31-JUL-2001 (first entry)

XX

DE

Human BCMA-Immunoglobulin G Fc region fusion construct.

XX

KW

Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;

KW

gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;

KW

carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;

KW

systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;

KW

B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;

KW

organ transplantation; HIV; human immunodeficiency virus; TNF; murine;

KW

tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;

KW

immunoglobulin G; IgG; Fc region.

XX

OS

Homo sapiens.

OS

Mus sp.

OS

Chimeric.



XX  
 FH Key Location/Qualifiers  
 FT Protein 1. .22  
 FT /label= Signal\_peptide  
 FT /note= "Derived from murine Ig kappa sequence"  
 FT Protein 23. .302  
 FT /label= Mature\_human\_BCMA\_IgG\_Fc\_fusion\_protein  
 FT Region 23. .75  
 FT /note= "Derived from human BCMA protein"  
 FT Domain 24. .302  
 FT /label= Cysteine\_rich\_domain  
 FT /note= "Derived from human BCMA"  
 FT Region 76. .302  
 FT /note= "Derived from human IgG Fc region"  
 XX  
 PN WO200124811-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027579.  
 XX  
 PR 06-OCT-1999; 99US-0157933P.  
 PR 11-FEB-2000; 2000US-0181807P.  
 PR 30-JUN-2000; 2000US-0215688P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA (APOT-) APOTECH R & D SA.  
 XX  
 PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;  
 XX  
 DR WPI; 2001-266242/27.  
 DR N-PSDB; AAD03847.  
 XX  
 PT Treating a mammal for a condition associated with undesired cell  
 PT proliferation such as cancer or carcinoma, comprises administering a  
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)  
 PT antagonist.  
 XX  
 PS Example 1; Fig 3B; 85pp; English.  
 XX  
 CC The invention relates to a method of treating a mammal for a condition  
 CC associated with undesired cell proliferation such as cancer or carcinoma.  
 CC The method involves administering a composition comprising A  
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell  
 CC maturation protein (BCM or BCMA) antagonist that antagonises the  
 CC interaction between APRIL and its cognate receptor(s). This method is  
 CC useful for treating undesired cell proliferation such as cancer or  
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,  
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated  
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's  
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular  
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,  
 CC immunosuppressive diseases, organ transplantation, inflammation and human  
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering  
 CC an immune response involving a signalling pathway between APRIL-R and its  
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence  
 CC is a fusion construct containing human APRIL-R also referred as BCMA or





```

      |||
Db      121 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 180
      |||
Qy      200 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 259
      |||
Db      181 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 240
      |||
Qy      260 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 302
      |||
Db      241 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 283

```

RESULT 4

AAE15489

ID AAE15489 standard; protein; 281 AA.

XX

AC AAE15489;

XX

DT 29-AUG-2003 (revised)

DT 12-MAR-2002 (first entry)

XX

DE Mouse BCMA-human immunoglobulin Fc region fusion protein.

XX

KW Human; transmembrane activator and intracellular CAML interactor; TACI;  
 KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
 KW rheumatoid arthritis; atherosclerosis; fusion protein; mouse.

XX

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX

PN WO200187979-A2.

XX

PD 22-NOV-2001.

XX

PF 14-MAY-2001; 2001WO-US015567.

XX

PR 12-MAY-2000; 2000US-0204039P.

PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.

XX

PA (AMGE-) AMGEN INC.

XX

PI Theill LE, Yu G;

XX

DR WPI; 2002-066686/09.

XX

PT Inhibiting activity of B cell maturation protein and/or transmembrane  
 PT activator and intracellular cyclophilin ligand interactor, by  
 PT administering a binding partner for APRIL, a tumor necrosis factor family  
 PT ligand.

XX

PS Disclosure; Fig 10B; 94pp; English.

XX

CC The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is mouse BCMA protein-human immunoglobulin Fc region fusion protein.  
CC (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 281 AA;

Query Match 85.1%; Score 1398.5; DB 5; Length 281;  
Best Local Similarity 92.2%; Pred. No. 8.3e-94;  
Matches 261; Conservative 4; Mismatches 9; Indels 9; Gaps 2;

Qy 27 MAGQCSQNEYFDSLHACIPCQLRCSNTPPLTCQRYCNASVTNSVKGV-----DKTH 79  
|| || :||||||| || |||: || || |: ||: ||| |||  
Db 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGSYTGSGGDKTH 58

Qy 80 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 139  
|||||||||||||||||||||||||||||||||||||||||||  
Db 59 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 118

Qy 140 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 199  
|||||||||||||||||||||||||||||||||||||||||||  
Db 119 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 178

Qy 200 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 259  
|||||||||||||||||||||||||||||||||||||||||||  
Db 179 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 238

Qy 260 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302  
|||||||||||||||||||||||||||||||||||||||||||  
Db 239 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 281

RESULT 5

AA014133

ID AA014133 standard; protein; 334 AA.

XX

AC AA014133;

XX

DT 29-AUG-2003 (revised)

DT 02-MAY-2002 (first entry)  
 XX  
 DE Protein of hTACI (32-114)-IgG1 Fc.  
 XX  
 KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;  
 KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;  
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;  
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;  
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;  
 KW scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;  
 KW lung fibrosis; uterine; a proliferation inducing ligand; chimeric;  
 KW hTACI(32-114)-IgG1 Fc.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .22  
 FT /note= "Signal peptide from murine IgG-kappa"  
 FT Domain 23. .105  
 FT /label= Extracellular\_domain  
 FT /note= "Human TACI extracellular domain"  
 FT Region 106. .334  
 FT /note= "hIgG1 Fc sequence"  
 XX  
 PN WO200181417-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 27-APR-2001; 2001WO-US040626.  
 XX  
 PR 27-APR-2000; 2000US-0199946P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA (APOT-) APOTEC R & D SA.  
 XX  
 PI Ambrose C, Thompson J, Schneider P, Rennert P;  
 XX  
 DR WPI; 2002-062027/08.  
 DR N-PSDB; AAK98729.  
 XX  
 PT Treating mammal for condition associated with undesired cell  
 PT proliferation e.g., solid tumor or reducing solid tumor size located in  
 PT mammal comprises administering transmembrane activator CAML interactor  
 PT protein reagent.  
 XX  
 PS Example; Fig 4; 42pp; English.  
 XX  
 CC This sequence represents the protein of a human TACI extracellular domain  
 CC with a truncated stalk region initiating after the second methionine  
 CC fused to human IgG Fc (hTACI(32-114)-IgG1 Fc). The signal sequence from  
 CC murine IgG-kappa was fused in frame with the human TACI extracellular  
 CC domain. The invention relates to treating a mammal for a condition  
 CC associated with undesired cell proliferation (e.g. a solid tumour, or  
 CC reducing the size of a solid tumour located on or in a mammal) comprising  
 CC administering a transmembrane activator CAML interactor protein (TACI)

CC reagent. The TACI reagent has cytostatic and vulnerary activity. Treating  
 CC a mammal (e.g. human, cow, horse, dog, mouse, rat or cat) for a condition  
 CC associated with undesired cell proliferation (e.g. cancer such as renal  
 CC cell cancer, Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma,  
 CC rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer,  
 CC mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous  
 CC cell carcinoma, gastrointestinal cancer or stomach cancer). The method is  
 CC also useful for treating cellular hyperproliferation (hyperplasia) such  
 CC as scleroderma, pannus formation in rheumatoid arthritis, post-surgical  
 CC scarring and lung, liver and uterine fibrosis. The TACI reagent of the  
 CC invention can extend mean survival time of a mammal by 25% as compared to  
 CC the mean survival time of a mammal in the absence of administering the  
 CC TACI reagent. The TACI reagent also reduces the size of the tumour by 25%  
 CC or more. (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 334 AA;

Query Match 83.9%; Score 1379; DB 5; Length 334;  
 Best Local Similarity 77.1%; Pred. No. 2.7e-92;  
 Matches 262; Conservative 10; Mismatches 24; Indels 44; Gaps 3;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | METDTLLLWVLLLWVPGSTG   | 56  |
|    |     |  |     |
| Db | 1   | METDTLLLWVLLLWVPGSTGDV                                       | 54  |
|    |     |  |     |
| Qy | 57  | -----PLTCQRYCNASVTNSVK-GVDKTHTCP                             | 82  |
|    |     |  |     |
| Db | 55  | AFCRSLSCRKEQGKFYDHLRDCISCASICGQHPKQCA                        | 114 |
|    |     |  |     |
| Qy | 83  | PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  | 142 |
|    |     |  |     |
| Db | 115 | PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  | 174 |
|    |     |  |     |
| Qy | 143 | KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ | 202 |
|    |     |  |     |
| Db | 175 | KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ | 234 |
|    |     |  |     |
| Qy | 203 | VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY | 262 |
|    |     |  |     |
| Db | 235 | VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY | 294 |
|    |     |  |     |
| Qy | 263 | SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK                     | 302 |
|    |     |  |     |
| Db | 295 | SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK                     | 334 |
|    |     |  |     |

RESULT 6

AAO14132

ID AAO14132 standard; protein; 366 AA.

XX

AC AAO14132;

XX

DT 29-AUG-2003 (revised)

DT 02-MAY-2002 (first entry)

XX

DE Protein of hTACI (1-114)-IgG1.

XX

KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;  
KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;  
KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;  
KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;  
KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;  
KW scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;  
KW lung fibrosis; uterine; a proliferation inducing ligand; hIgG1 Fc; IgG1;  
KW hTACI; chimeric.

XX

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Peptide 1. .23

FT /note= "Signal peptide from murine IgG-kappa"

FT Domain 24. .137

FT /label= Extracellular\_domain

FT /note= "Human TACI extracellular domain"

FT Region 138. .366

FT /note= "hIgG1 Fc sequence"

XX

PN WO200181417-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US040626.

XX

PR 27-APR-2000; 2000US-0199946P.

XX

PA (BIOJ ) BIOGEN INC.

PA (APOT-) APOTEC R & D SA.

XX

PI Ambrose C, Thompson J, Schneider P, Rennert P;

XX

DR WPI; 2002-062027/08.

DR N-PSDB; AAK98728.

XX

PT Treating mammal for condition associated with undesired cell  
PT proliferation e.g., solid tumor or reducing solid tumor size located in  
PT mammal comprises administering transmembrane activator CAML interactor  
PT protein reagent.

XX

PS Disclosure; Fig 3; 42pp; English.

XX

CC This sequence represents the protein of a human TACI extracellular domain  
CC with a truncated stalk region fused to human IgG Fc, called hTACI (1-114)  
CC -IgG1. The signal sequence from murine IgG-kappa was fused in frame with  
CC the human TACI extracellular domain. The invention relates to treating a  
CC mammal for a condition associated with undesired cell proliferation (e.g.  
CC a solid tumour, or reducing the size of a solid tumour located on or in a  
CC mammal) comprising administering a transmembrane activator CAML  
CC interactor protein (TACI) reagent. The TACI reagent has cytostatic and  
CC vulnery activity. Treating a mammal (e.g. human, cow, horse, dog,  
CC mouse, rat or cat) for a condition associated with undesired cell  
CC proliferation (e.g. cancer such as renal cell cancer, Kaposi's sarcoma,  
CC breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer,



CC melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary  
 CC adenocarcinoma, pharyngeal squamous cell carcinoma, gastrointestinal  
 CC cancer or stomach cancer). The method is also useful for treating  
 CC cellular hyperproliferation (hyperplasia) such as scleroderma, pannus  
 CC formation in rheumatoid arthritis, post-surgical scarring and lung, liver  
 CC and uterine fibrosis. The TACI reagent of the invention can extend mean  
 CC survival time of a mammal by 25% as compared to the mean survival time of  
 CC a mammal in the absence of administering the TACI reagent. The TACI  
 CC reagent also reduces the size of the tumour by 25% or more. (Updated on  
 CC 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 366 AA;

Query Match 83.7%; Score 1376; DB 5; Length 366;  
 Best Local Similarity 72.1%; Pred. No. 5e-92;  
 Matches 264; Conservative 11; Mismatches 27; Indels 64; Gaps 3;

```

Qy      1 METDTLLLWVLLLWVPGSTGDVTMLQMA-----GQCSQN 34
      |||||
Db      1 METDTLLLWVLLLWVPGSTGDVTMSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEE 60

Qy     35 EYFDSLHACIPCQLRCSSNTP-----P 57
      :|:| || |: |: |: :
Db     61 QYWDPELLGTCMSCKTICNHQSQRTCAAFCSRSLSCRKEQGKFYDHLRDCISCASICGQHP 120

Qy     58 LTCQRYCNASVTNSVK-GVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 116
      | :| : : | |||
Db    121 KQCAYFCENKLRSFVNLPVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 180

Qy    117 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 176
      |||||
Db    181 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 240

Qy    177 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 236
      |||||
Db    241 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 300

Qy    237 ESNQGPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 296
      |||||
Db    301 ESNQGPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 360

Qy    297 SLSPGK 302
      |||||
Db    361 SLSPGK 366

```

# RESULT 7

AAE22245

ID AAE22245 standard; protein; 320 AA.

XX

AC AAE22245;

XX

DT 29-AUG-2003 (revised)

DT 25-JUL-2002 (first entry)

XX

DE Murine IgG-kappa signal sequence-human BAFF-R:Fc fusion protein.

XX

KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;  
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;  
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;  
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;  
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;  
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;  
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;  
 KW murine; immunoglobulin G; IgG; fusion protein.  
 XX  
 OS Homo sapiens.  
 OS Mus musculus.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .21  
 FT /label= Signal\_peptide  
 FT /note= "Murine IgG-kappa signal sequence"  
 FT Protein 22. .320  
 FT /note= "Mature human BAFF-R:Fc protein"  
 FT Misc-difference 22  
 FT /note= "Encoded by region introducing restriction site"  
 FT Domain 23. .92  
 FT /note= "Human BAFF-R extracellular domain"  
 FT Misc-difference 93  
 FT /note= "Encoded by region introducing restriction site"  
 FT Region 94. .320  
 FT /note= "Human IgG1 Fc region"  
 XX  
 PN WO200224909-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 06-SEP-2001; 2001WO-US028006.  
 XX  
 PR 18-SEP-2000; 2000US-0233152P.  
 PR 21-SEP-2000; 2000US-0234140P.  
 PR 13-FEB-2001; 2001US-0268499P.  
 PR 14-AUG-2001; 2001US-0312185P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Ambrose CM, Thompson JS;  
 XX  
 DR WPI; 2002-362428/39.  
 DR N-PSDB; AAD35412.  
 XX  
 PT New human BAFF receptor proteins and nucleic acids, useful for treating,  
 PT preventing or delaying e.g. autoimmune diseases, cancers, inherited  
 PT genetic disorders involving B-cells, cardiovascular disorders, or renal  
 PT disorders.  
 XX  
 PS Example 9; Fig 9; 164pp; English.  
 XX  
 CC The invention relates to human BAFF receptor (BAFF-R) nucleic acids and  
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour  
 CC Necrosis Factor (TNF) family, which is associated with the expression of  
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are



AC ABR55865;  
 XX  
 DT 02-SEP-2003 (first entry)  
 XX  
 DE Human immunoglobulin G (IgG) Fc portion.  
 XX  
 KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;  
 KW immunoglobulin G; IgG; Fc; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003031464-A2.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 09-OCT-2002; 2002WO-US032263.  
 XX  
 PR 10-OCT-2001; 2001US-0328523P.  
 PR 19-OCT-2001; 2001US-0344692P.  
 PR 28-NOV-2001; 2001US-0334233P.  
 PR 28-NOV-2001; 2001US-0334301P.  
 PR 07-JUN-2002; 2002US-0387292P.  
 PR 25-JUN-2002; 2002US-0391777P.  
 PR 17-JUL-2002; 2002US-0396594P.  
 PR 16-AUG-2002; 2002US-0404249P.  
 PR 28-AUG-2002; 2002US-0407527P.  
 XX  
 PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 XX  
 PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;  
 XX  
 DR WPI; 2003-449162/42.  
 DR N-PSDB; ACC78891.  
 XX  
 PT Remodeling a peptide, by removing a saccharyl subunit from the peptide to  
 PT form truncated glycan, and adding or deleting glycosyl groups to a  
 PT peptide and/or adding modifying group of a peptide to remodel the  
 PT peptide.  
 XX  
 PS Example; Fig 75B; 900pp; English.  
 XX  
 CC The invention relates to a cell-free, in vitro method of remodeling a  
 CC peptide. The method involves removing a saccharyl subunit from the  
 CC peptide, thus forming a truncated glycan, and contacting the truncated  
 CC glycan with at least one glycosyltransferase and at least one glycosyl  
 CC donor under conditions suitable to transfer at least one glycosyl donor  
 CC to the truncated glycan, thus remodeling the peptide. Conjugates can be  
 CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,  
 CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,  
 CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin  
 CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)  
 CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)  
 CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)  
 CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha  
 CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-  
 CC glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2  
 CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-

CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,  
 CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth  
 CC hormone (HGH) peptide, and a modifying group, where the modifying group  
 CC is covalently attached to the peptide through an intact glycosyl linking  
 CC group. The method is useful for a cell-free, in vitro method of  
 CC remodeling the above mentioned peptides. The present sequence represents  
 CC a human immunoglobulin G (IgG) Fc portion  
 XX  
 SQ Sequence 320 AA;

Query Match 82.8%; Score 1361; DB 6; Length 320;  
 Best Local Similarity 82.2%; Pred. No. 5.2e-91;  
 Matches 263; Conservative 5; Mismatches 34; Indels 18; Gaps 3;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | METDTLLLWVLLLWVPGSTGDVTM--LQMAQQ-----CSQNEYFDSLHACIPCQL--    | 49  |
|    |     | :   :       :   :  |     |
| Db | 1   | METDTLLLWVLLLWVPGSTGDVRRGPRSLRGRDAPAPTPCVPAECFDLLVRHCVACGLLR | 60  |
| Qy | 50  | -----RCSSNTPPLTCQRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKP   | 102 |
|    |     | :  |     |
| Db | 61  | TPRPKPAGASSPAPRTALQPQESVGAGAGEAAVDKTHTCPPCPAPELLGGPSVFLFPPKP | 120 |
| Qy | 103 | KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT | 162 |
|    |     |  |     |
| Db | 121 | KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT | 180 |
| Qy | 163 | VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT  | 222 |
|    |     |  |     |
| Db | 181 | VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT  | 240 |
| Qy | 223 | LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC    | 282 |
|    |     |  |     |
| Db | 241 | LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC    | 300 |
| Qy | 283 | MHEALHNHYTQKSLSLSPGK   | 302 |
|    |     |  |     |
| Db | 301 | MHEALHNHYTQKSLSLSPGK   | 320 |

# RESULT 9

AAE35228

ID AAE35228 standard; protein; 332 AA.

XX

AC AAE35228;

XX

DT 23-OCT-2003 (revised)

DT 28-MAY-2003 (first entry)

XX

DE Human TACI-Fc5 fusion protein comprising murine 26-10 VH signal peptide.

XX

KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;  
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;  
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;  
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;  
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;  
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;  
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;



Db 122 APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 181  
 Qy 152 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 211  
 Db 182 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQVYTLPPSRD 241  
 Qy 212 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 271  
 Db 242 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 301  
 Qy 272 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302  
 Db 302 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332

RESULT 10

AAE13055

ID AAE13055 standard; protein; 446 AA.

XX

AC AAE13055;

XX

DT 28-JAN-2002 (first entry)

XX

DE ADAM-17dis-Fc fusion construct.

XX

KW Human; ADAM disintegrin domain; integrin; endothelial cell migration;  
 KW angiogenesis; ocular disorder; inflammatory disease; bone resorption;  
 KW osteoporosis; restenosis; thrombosis; tissue repair; wound healing;  
 KW retinopathy; retinoblastoma; neovascular glaucoma; macular degeneration;  
 KW retrolental fibroplasia; inflammatory bowel disease; rubeosis; uveitis;  
 KW arthritis; rheumatism; myocardial infarction; coronary artery disease;  
 KW tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;  
 KW preeclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;  
 KW IgK; Fc region; antiinflammatory; osteopathic; vasotropic; thrombolytic.

XX

OS Homo sapiens.

OS Unidentified.

OS Chimeric.

XX

| FH | Key     | Location/Qualifiers                            |
|----|---------|--|
| FT | Peptide | 1. .20   |
| FT |         | /label= IgK_leader_sequence                    |
| FT | Protein | 21. .446                                       |
| FT |         | /note= "Mature ADAM-17dis-Fc fusion construct" |
| FT | Region  | 23. .216                                       |
| FT |         | /note= "Human ADAM disintegrin"                |
| FT | Domain  | 34. .93  |
| FT |         | /label= Human_ADAM_disintegrin_domain          |
| FT | Region  | 219. .446                                      |
| FT |         | /note= "Fc region"                             |

XX

PN WO200162905-A2.

XX

PD 30-AUG-2001.

XX

PF 23-FEB-2001; 2001WO-US005701.

XX

PR 25-FEB-2000; 2000US-0184865P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Fanslow WC, Cerretti DP, Poindexter KM, Black RA;

XX

DR WPI; 2001-625725/72.

DR N-PSDB; AAD21435.

XX

PT Antagonizing the binding of an integrin to its ligand useful for the  
PT treatment of angiogenesis comprises administration of an ADAM-disintegrin  
PT domain polypeptide.

XX

PS Claim 11; Page 46-47; 66pp; English.

XX

CC The invention relates to the method and use of ADAM disintegrin domain  
CC polypeptides for inhibiting the biological activity of integrins,  
CC endothelial cell migration and angiogenesis. ADAM disintegrin domain  
CC polypeptides are used for treatment of ocular disorders, malignant and  
CC metastatic conditions, inflammatory diseases, osteoporosis and other  
CC conditions mediated by accelerated bone resorption, restenosis,  
CC inappropriate platelet activation, recruitment or aggregation, thrombosis  
CC or a condition requiring aggregation, thrombosis or a condition requiring  
CC tissue repair or wound healing, angiogenesis, ocular neovascularisation  
CC or solid tumour, diabetic retinopathy, retinopathy or prematurity,  
CC neovascular glaucoma, retinoblastoma, retrolental fibroplasias, rubeosis,  
CC uveitis, macular degeneration and corneal graft neovascularisation,  
CC inflammatory diseases, ocular tumours, diseases associated with choroidal  
CC or iris neovascularisation, arthritis, rheumatism, inflammatory bowel  
CC disease, psoriasis, coronary artery disease or injury, myocardial  
CC infarction or injury following myocardial infarction, stroke, unstable  
CC angina, atherosclerosis, arteriosclerosis, preeclampsia, embolism,  
CC platelet-associated ischaemic disorders including lung ischaemia,  
CC coronary ischaemia, cerebral ischaemia, restenosis following percutaneous  
CC coronary intervention including angioplasty, atherectomy, stent placement  
CC and bypass surgery, thrombotic disorders including coronary artery  
CC thrombosis, cerebral artery thrombosis, intracardiac thrombosis,  
CC peripheral artery thrombosis, venous thrombosis, thrombosis and  
CC coagulopathies associated with exposure to a foreign or injured tissue  
CC surface and reocclusion following thrombosis, deep venous thrombosis,  
CC pulmonary embolism, transient ischaemic attacks and another conditions  
CC where vascular occlusion is a common underlying feature, in individuals  
CC at high risk for thrombus formation of reformation, advanced coronary  
CC artery disease, or for occlusion, reocclusion, stenosis and/or restenosis  
CC of blood vessels or stroke benign tumours and preneoplastic conditions,  
CC myocardial angiogenesis, haemophilic joints, scleroderma, vascular  
CC adhesions, asthma and allergy, eczema and dermatitis, graft versus host  
CC disease, sepsis, adult respiratory distress syndrome, telangiectasia and  
CC wound granulation. The method are used in combination with angioplasty  
CC procedures, such as balloon angioplasty, laser angioplasty, coronary  
CC atherectomy or similar techniques, carotid endarterectomy, anastomosis of  
CC vascular grafts, surgery having a high risk of thrombus formation (i.e.  
CC coronary bypass surgery, insertion of a prosthetic valve or vessel and  
CC the like), atherectomy, stent placement, placement of a chronic  
CC cardiovascular device such as an in-dwelling catheter or prosthetic valve  
CC or vessel, organ transplantation or bypass surgery. The present sequence  
CC is ADAM disintegrin domain polypeptide fusion construct. The fusion



CC construct comprises of immunoglobulin K (IgK) leader, human ADAM  
 CC disintegrin and Fc region  
 XX  
 SQ Sequence 446 AA;

Query Match 77.2%; Score 1269; DB 4; Length 446;  
 Best Local Similarity 57.2%; Pred. No. 3.9e-84;  
 Matches 261; Conservative 2; Mismatches 29; Indels 164; Gaps 5;

```

Qy      1 METDTLLLWVLLLWVPGSTG-----DVTMLQMAQC 31
      |||
Db      1 METDTLLLWVLLLWVPGSTGTSCGNSRVDEGEEDPGIMYLNNDTCCNSDCT-LKEGVQC 59
      |||

Qy     32 SQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNAS----- 67
      |
Db     60 SDRN-----SPCKKNCQFETAQKKCQEAINATCKGVSCTGNSSECPPPGNAEDDT 110
      ||

Qy     68 -----VTNSVK----- 73
      ||
Db    111 VCLDLGKCKDGKCI PFCEREQQLESCACNETDNSCKVCCRDLSGRCVPYVDAEQKNLFLR 170
      ||

Qy     74 -----GVDKTHTCPPCPA 86
      |||
Db    171 KGKPCTVGFCDMNGKCEKRVQDVIERFWDFIDQLSINTFGKFLADNRSCDKTHTCPPCPA 230
      |||

Qy     87 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 146
      ||
Db    231 PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 290
      |||

Qy    147 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 206
      |||
Db    291 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 350
      |||

Qy    207 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 266
      |||
Db    351 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 410
      |||

Qy    267 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
      |||
Db    411 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 446
      |||

```

# RESULT 11

AAAY84965

ID AAY84965 standard; protein; 633 AA.

XX

AC AAY84965;

XX

DT 21-AUG-2000 (first entry)

XX

DE Amino acid sequence of a CD-20 specific chimeric receptor.

XX

KW CD20-specific receptor; CD-20 specific redirected T cell; leukemia;

KW CD20+ malignancy; non-Hodgkin's lymphoma; myeloablative chemotherapy;

KW stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis.

XX

OS Synthetic.

OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 21. .126  
 FT /note= "anti-CD20 variable regions"  
 FT Peptide 27. .86  
 FT /note= "signal peptide from murine T86.66 antibody kappa  
 FT light chain"  
 FT Peptide 145. .266  
 FT /note= "GS18 linker"  
 FT Region 283. .392  
 FT /note= "hinge region"  
 FT Region 393. .499  
 FT /note= "CH3 region"  
 FT Region 500. .521  
 FT /note= "CD4 transmembrane region"  
 FT Region 522. .633  
 FT /note= "zeta chain"  
 XX  
 PN WO200023573-A2.  
 XX  
 PD 27-APR-2000.  
 XX  
 PF 20-OCT-1999; 99WO-US024484.  
 XX  
 PR 20-OCT-1998; 98US-0105014P.  
 XX  
 PA (CITY ) CITY OF HOPE.  
 XX  
 PI Raubitschek A, Jensen MC, Wu AM;  
 XX  
 DR WPI; 2000-339676/29.  
 DR N-PSDB; AAA15019.  
 XX  
 PT Genetically engineered CD20-specific redirected T cells useful for  
 PT treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+  
 PT acute or chronic leukemia, and autoimmune disease.  
 XX  
 PS Claim 10; Page 53-55; 58pp; English.  
 XX  
 CC The present sequence represents a synthetic CD20-specific chimeric  
 CC receptor. The specification describes CD-20 specific redirected T cells  
 CC which express and bear on the cell surface membrane a CD20-chimeric  
 CC receptor comprising an intracellular signalling domain, a transmembrane  
 CC domain and an extracellular domain, the extracellular domain comprising a  
 CC CD20-specific receptor. The genetically engineered CD20-specific  
 CC redirected T cells are useful for treating a CD20+ malignancy, such as  
 CC non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a human  
 CC patient having previously undergone myeloablative chemotherapy and stem  
 CC cell rescue. The genetically engineered CD20-specific redirected T cells  
 CC are also useful for abrogating an untoward B cell function, such as  
 CC autoimmune disease (lupus or rheumatoid arthritis) in a patient  
 XX  
 SQ Sequence 633 AA;

Query Match 77.2%; Score 1268.5; DB 3; Length 633;  
 Best Local Similarity 53.1%; Pred. No. 6.4e-84;

|    | Matches | 265;  | Conservative | 9;    | Mismatches | 28;   | Indels | 197;   | Gaps    | 5;      |
|----|---------|-------|--------------|-------|------------|-------|--------|--------|---------|---------|
| Qy | 1       | METD  | LLLLWV       | LLLV  | PGST       | GDVT  | MLQM   | AGQCSQ | NE----- | 35      |
|    |         |       |              |       |            |       |        |        |         |         |
| Db | 1       | METD  | LLLLWV       | LLLV  | PGST       | GDIV  | LTQSP  | AILSAS | PGKVTMT | CRASSSV |
|    |         |       |              |       |            |       |        |        |         | NYMDWY  |
|    |         |       |              |       |            |       |        |        |         | QKKPG   |
|    |         |       |              |       |            |       |        |        |         | 60      |
| Qy | 36      | ----- | YFDS         | LLHAC | IP-----    |       |        |        | CQ----- | 48      |
|    |         |       |              |       |            | :     | :      |        |         |         |
| Db | 61      | SSPK  | PWIYAT       | SNLAS | GVPAR      | FSGSG | SGTSY  | SLTISR | VEAEDA  | ATYYCQ  |
|    |         |       |              |       |            |       |        |        |         | QWFSN   |
|    |         |       |              |       |            |       |        |        |         | PPPTFG  |
|    |         |       |              |       |            |       |        |        |         | GGG     |
|    |         |       |              |       |            |       |        |        |         | 120     |
| Qy | 49      | ----- |              |       |            |       |        |        |         | 48      |
| Db | 121     | TKLE  | IKGST        | SGGG  | SGGG       | SGGG  | SGGG   | SSVQL  | QQSGA   | ELVKP   |
|    |         |       |              |       |            |       |        |        |         | GASVK   |
|    |         |       |              |       |            |       |        |        |         | MSCKA   |
|    |         |       |              |       |            |       |        |        |         | SGYTFT  |
|    |         |       |              |       |            |       |        |        |         | SYNMHW  |
|    |         |       |              |       |            |       |        |        |         | 180     |
| Qy | 49      | ----- |              |       |            |       |        |        | LRCS    | SNTPPL  |
|    |         |       |              |       |            |       |        |        |         | TCQRYC  |
|    |         |       |              |       |            |       |        |        |         | 64      |
| Db | 181     | VKQT  | PGQGLE       | WIGAI | YPGN       | GDTSY | NQKFK  | GKATLT | ADKSSS  | TAYMQL  |
|    |         |       |              |       |            |       |        |        |         | SSSLT   |
|    |         |       |              |       |            |       |        |        |         | SEDSAD  |
|    |         |       |              |       |            |       |        |        |         | YYC     |
|    |         |       |              |       |            |       |        |        |         | 240     |
| Qy | 65      | ----- | NASV         | TNSV  | -----      | KGVD  | KTHTC  | PPCPA  | PELLG   | GPSVFL  |
|    |         |       |              |       | :          |       |        |        |         |         |
| Db | 241     | ARSN  | YGYSS        | YWF   | FDVW       | GAGT  | TVT    | VSSLD  | PKSSD   | KTHTC   |
|    |         |       |              |       |            |       |        |        |         | PPCPA   |
|    |         |       |              |       |            |       |        |        |         | PELLG   |
|    |         |       |              |       |            |       |        |        |         | GPSVFL  |
|    |         |       |              |       |            |       |        |        |         | FPPKPK  |
|    |         |       |              |       |            |       |        |        |         | 300     |
| Qy | 104     | DTLM  | ISRTPE       | VT    | CVV        | VDV   | SHED   | PEVK   | FNWY    | VDGVE   |
|    |         |       |              |       |            |       |        |        |         | VHNAK   |
|    |         |       |              |       |            |       |        |        |         | TKPRE   |
|    |         |       |              |       |            |       |        |        |         | EQYNST  |
|    |         |       |              |       |            |       |        |        |         | YRVVSV  |
|    |         |       |              |       |            |       |        |        |         | LT      |
|    |         |       |              |       |            |       |        |        |         | 163     |
| Db | 301     | DTLM  | ISRTPE       | VT    | CVV        | VDV   | SHED   | PEVK   | FNWY    | VDGVE   |
|    |         |       |              |       |            |       |        |        |         | VHNAK   |
|    |         |       |              |       |            |       |        |        |         | TKPRE   |
|    |         |       |              |       |            |       |        |        |         | EQYNST  |
|    |         |       |              |       |            |       |        |        |         | YRVVSV  |
|    |         |       |              |       |            |       |        |        |         | LT      |
|    |         |       |              |       |            |       |        |        |         | 360     |
| Qy | 164     | LHQD  | WLNGKE       | YKCK  | VSNK       | ALPA  | PIEKT  | ISKAK  | GQPRE   | PQVYTL  |
|    |         |       |              |       |            |       |        |        |         | PPSRDE  |
|    |         |       |              |       |            |       |        |        |         | LTKNQV  |
|    |         |       |              |       |            |       |        |        |         | SLTCL   |
|    |         |       |              |       |            |       |        |        |         | 223     |
| Db | 361     | LHQD  | WLNGKE       | YKCK  | VSNK       | ALPA  | PIEKT  | ISKAK  | GQPRE   | PQVYTL  |
|    |         |       |              |       |            |       |        |        |         | PPSRDE  |
|    |         |       |              |       |            |       |        |        |         | LTKNQV  |
|    |         |       |              |       |            |       |        |        |         | SLTCL   |
|    |         |       |              |       |            |       |        |        |         | 420     |
| Qy | 224     | VKGF  | YPSDIA       | VEWES | NGQP       | ENNYK | TPPV   | LDS    | DGSS    | FFLYSK  |
|    |         |       |              |       |            |       |        |        |         | LTVDK   |
|    |         |       |              |       |            |       |        |        |         | SRWQQ   |
|    |         |       |              |       |            |       |        |        |         | GNVFSC  |
|    |         |       |              |       |            |       |        |        |         | SVM     |
|    |         |       |              |       |            |       |        |        |         | 283     |
| Db | 421     | VKGF  | YPSDIA       | VEWES | NGQP       | ENNYK | TPPV   | LDS    | DGSS    | FFLYSK  |
|    |         |       |              |       |            |       |        |        |         | LTVDK   |
|    |         |       |              |       |            |       |        |        |         | SRWQQ   |
|    |         |       |              |       |            |       |        |        |         | GNVFSC  |
|    |         |       |              |       |            |       |        |        |         | SVM     |
|    |         |       |              |       |            |       |        |        |         | 480     |
| Qy | 284     | HEAL  | HNHYTQ       | KSLS  | LSPGK      |       |        |        |         |         |
|    |         |       |              |       |            |       |        |        |         | 302     |
| Db | 481     | HEAL  | HNHYTQ       | KSLS  | LSPGK      |       |        |        |         |         |
|    |         |       |              |       |            |       |        |        |         | 499     |

# RESULT 12

AAE13053

ID AAE13053 standard; protein; 465 AA.

XX

AC AAE13053;

XX

DT 28-JAN-2002 (first entry)

XX

DE ADAM-10dis-Fc fusion construct.

XX

KW Human; ADAM disintegrin domain; integrin; endothelial cell migration;

KW angiogenesis; ocular disorder; inflammatory disease; bone resorption;

KW osteoporosis; restenosis; thrombosis; tissue repair; wound healing;

KW retinopathy; retinoblastoma; neovascular glaucoma; macular degeneration;

KW retrolental fibroplasia; inflammatory bowel disease; rubeosis; uveitis;

KW arthritis; rheumatism; myocardial infarction; coronary artery disease;

KW tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;

KW preeclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;

KW IgK; Fc region; antiinflammatory; osteopathic; vasotropic; thrombolytic.  
 XX  
 OS Homo sapiens.  
 OS Unidentified.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .20  
 FT /label= IgK\_leader\_sequence  
 FT Protein 21. .465  
 FT /note= "Mature ADAM-10dis-Fc fusion construct"  
 FT Region 23. .235  
 FT /note= "Human ADAM disintegrin"  
 FT Domain 34. .99  
 FT /label= Human\_ADAM\_disintegrin\_domain  
 FT Region 238. .465  
 FT /note= "Fc region"  
 XX  
 PN WO200162905-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-US005701.  
 XX  
 PR 25-FEB-2000; 2000US-0184865P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Fanslow WC, Cerretti DP, Poindexter KM, Black RA;  
 XX  
 DR WPI; 2001-625725/72.  
 DR N-PSDB; AAD21433.  
 XX  
 PT Antagonizing the binding of an integrin to its ligand useful for the  
 PT treatment of angiogenesis comprises administration of an ADAM-disintegrin  
 PT domain polypeptide.  
 XX  
 PS Claim 11; Page 40-41; 66pp; English.  
 XX  
 CC The invention relates to the method and use of ADAM disintegrin domain  
 CC polypeptides for inhibiting the biological activity of integrins,  
 CC endothelial cell migration and angiogenesis. ADAM disintegrin domain  
 CC polypeptides are used for treatment of ocular disorders, malignant and  
 CC metastatic conditions, inflammatory diseases, osteoporosis and other  
 CC conditions mediated by accelerated bone resorption, restenosis,  
 CC inappropriate platelet activation, recruitment or aggregation, thrombosis  
 CC or a condition requiring aggregation, thrombosis or a condition requiring  
 CC tissue repair or wound healing, angiogenesis, ocular neovascularisation  
 CC or solid tumour, diabetic retinopathy, retinopathy or prematurity,  
 CC neovascular glaucoma, retinoblastoma, retrolental fibroplasias, rubeosis,  
 CC uveitis, macular degeneration and corneal graft neovascularisation,  
 CC inflammatory diseases, ocular tumours, diseases associated with choroidal  
 CC or iris neovascularisation, arthritis, rheumatism, inflammatory bowel  
 CC disease, psoriasis, coronary artery disease or injury, myocardial  
 CC infarction or injury following myocardial infarction, stroke, unstable  
 CC angina, atherosclerosis, arteriosclerosis, preeclampsia, embolism,  
 CC platelet-associated ischaemic disorders including lung ischaemia,

CC coronary ischaemia, cerebral ischaemia, restenosis following percutaneous  
 CC coronary intervention including angioplasty, atherectomy, stent placement  
 CC and bypass surgery, thrombotic disorders including coronary artery  
 CC thrombosis, cerebral artery thrombosis, intracardiac thrombosis,  
 CC peripheral artery thrombosis, venous thrombosis, thrombosis and  
 CC coagulopathies associated with exposure to a foreign or injured tissue  
 CC surface and reocclusion following thrombosis, deep venous thrombosis,  
 CC pulmonary embolism, transient ischaemic attacks and another conditions  
 CC where vascular occlusion is a common underlying feature, in individuals  
 CC at high risk for thrombus formation of reformation, advanced coronary  
 CC artery disease, or for occlusion, reocclusion, stenosis and/or restenosis  
 CC of blood vessels or stroke benign tumours and preneoplastic conditions,  
 CC myocardial angiogenesis, haemophilic joints, scleroderma, vascular  
 CC adhesions, asthma and allergy, eczema and dermatitis, graft versus host  
 CC disease, sepsis, adult respiratory distress syndrome, telangiectasia and  
 CC wound granulation. The method are used in combination with angioplasty  
 CC procedures, such as balloon angioplasty, laser angioplasty, coronary  
 CC atherectomy or similar techniques, carotid endarterectomy, anastomosis of  
 CC vascular grafts, surgery having a high risk of thrombus formation (i.e.  
 CC coronary bypass surgery, insertion of a prosthetic valve or vessel and  
 CC the like), atherectomy, stent placement, placement of a chronic  
 CC cardiovascular device such as an in-dwelling catheter or prosthetic valve  
 CC or vessel, organ transplantation or bypass surgery. The present sequence  
 CC is ADAM disintegrin domain polypeptide fusion construct. The fusion  
 CC construct comprises of immunoglobulin K (IgK) leader, human ADAM  
 CC disintegrin and Fc region  
 XX  
 SQ Sequence 465 AA;

Query Match 77.0%; Score 1265.5; DB 4; Length 465;  
 Best Local Similarity 56.1%; Pred. No. 7.3e-84;  
 Matches 261; Conservative 11; Mismatches 30; Indels 163; Gaps 7;

```

Qy      1 METDTLLLWVLLLWVPGSTG-----DVTM-----L 25
          |||||
Db      1 METDTLLLWVLLLWVPGSTGTSCNGMVEQGEEDCGYSQCKDECCFDANQPEGRKCKL 60

Qy      26 QMAGQCSQNE-----YFDSLHACIP----- 46
          : ||| ::
Db      61 KPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDCAREGICNGFTALCPASDEKPNFTDCNR 120

Qy      47 -----CQLRCSSNTPPLTC----- 60
          | : | | ||
Db      121 HTQVCINGQCAGSICEKYGLEECTCASSDGKDDKELCHVCCMKMDPSTCASTGSVQWSR 180

Qy      61 -----QRYCN-----ASVTNSV-----KGVDK 77
          : ||: | : :: : ||
Db      181 HFSGRITITLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKKAI FSPELYENIAERSCDK 240

Qy      78 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV 137
          |||||
Db      241 THTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV 300

Qy      138 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 197
          |||||
Db      301 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 360

```

Qy 198 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 257  
 |||  
 Db 361 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 420  
 Qy 258 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302  
 |||  
 Db 421 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465

RESULT 13

AAO14136

ID AAO14136 standard; protein; 404 AA.

XX

AC AAO14136;

XX

DT 29-AUG-2003 (revised)

DT 02-MAY-2002 (first entry)

XX

DE Protein of a complete TACI extracellular domain fused to a human IgG-Fc.

XX

KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;  
 KW cell proliferation; tumour; vulnerary; renal cell cancer; mastocytoma;  
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;  
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;  
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;  
 KW scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;  
 KW lung fibrosis; uterine; IgG-Fc; chimeric.

XX

OS Homo sapiens.

OS Chimeric.

XX

PN WO200181417-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US040626.

XX

PR 27-APR-2000; 2000US-0199946P.

XX

PA (BIOJ ) BIOGEN INC.

PA (APOT-) APOTECH R & D SA.

XX

PI Ambrose C, Thompson J, Schneider P, Rennert P;

XX

DR WPI; 2002-062027/08.

DR N-PSDB; AAK98732.

XX

PT Treating mammal for condition associated with undesired cell  
 PT proliferation e.g., solid tumor or reducing solid tumor size located in  
 PT mammal comprises administering transmembrane activator CAML interactor  
 PT protein reagent.

XX

PS Example; Fig 5; 42pp; English.

XX

CC This sequence represents the protein of a complete extracellular domain  
 CC of TACI fused to a human IgG-Fc. The invention relates to treating a  
 CC mammal for a condition associated with undesired cell proliferation (e.g.

CC a solid tumour, or reducing the size of a solid tumour located on or in a  
 CC mammal) comprising administering a transmembrane activator CAML  
 CC interactor protein (TACI) reagent. The TACI reagent has cytostatic and  
 CC vulnerary activity. Treating a mammal (e.g. human, cow, horse, dog,  
 CC mouse, rat or cat) for a condition associated with undesired cell  
 CC proliferation (e.g. cancer such as renal cell cancer, Kaposi's sarcoma,  
 CC breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer,  
 CC melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary  
 CC adenocarcinoma, pharyngeal squamous cell carcinoma, gastrointestinal  
 CC cancer or stomach cancer). The method is also useful for treating  
 CC cellular hyperproliferation (hyperplasia) such as scleroderma, pannus  
 CC formation in rheumatoid arthritis, post-surgical scarring and lung, liver  
 CC and uterine fibrosis. The TACI reagent of the invention can extend mean  
 CC survival time of a mammal by 25% as compared to the mean survival time of  
 CC a mammal in the absence of administering the TACI reagent. The TACI  
 CC reagent also reduces the size of the tumour by 25% or more. (Updated on  
 CC 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 404 AA;

Query Match 77.0%; Score 1264.5; DB 5; Length 404;  
 Best Local Similarity 77.7%; Pred. No. 7.3e-84;  
 Matches 244; Conservative 6; Mismatches 19; Indels 45; Gaps 3;

```

Qy      33 QNEYFDSLHACIPC-----QLRCSSNTPPLTCQRYCNASVTN----- 70
      |::| || || | :|| || | :| : ||
Db      92 QGKFYDHLRDCISCASICGQHPKQCA YFCENKLRSPVNLPP-ELRRQRSGEVENNSDNS 150

Qy      71 -----SVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 108
      | |||||
Db     151 GRYQGLEHRGSEASPALPGLKLSADQVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 210

Qy     109 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 168
      |||||
Db     211 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 270

Qy     169 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 228
      |||||
Db     271 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 330

Qy     229 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALH 288
      |||||
Db     331 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALH 390

Qy     289 NHYTQKSLSLSPGK 302
      |||||
Db     391 NHYTQKSLSLSPGK 404

```

RESULT 14

AAE35225

ID AAE35225 standard; protein; 348 AA.

XX

AC AAE35225;

XX

DT 28-MAY-2003 (first entry)

XX

DE Human TACI(dl-29, dl111-154)-Fc5 variant construct protein.

XX

KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;  
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;  
KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;  
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;  
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;  
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;  
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;  
KW chimeric.

XX

OS Homo sapiens.

XX

PN WO200294852-A2.

XX

PD 28-NOV-2002.

XX

PF 20-MAY-2002; 2002WO-US015910.

XX

PR 24-MAY-2001; 2001US-0293343P.

XX

PA (ZYMO ) ZYMOGENETICS INC.

XX

PI Rixon MW, Gross JA;

XX

DR WPI; 2003-148455/14.

DR

N-PSDB; AAD53772.

XX

PT Transmembrane activator and calcium modulator and cyclophilin ligand-  
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or  
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.

XX

PS Claim 26; Col 129-130; 71pp; English.

XX

CC The invention relates to fusion proteins comprising transmembrane  
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)  
CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or  
CC ZTNF4; and an immunoglobulin group comprising a constant region of an  
CC immunoglobulin. The invention is used to manufacture a medicament for  
CC inhibiting the proliferation of tumour cells in a mammalian subject. The  
CC composition comprising the fusion protein may also be used in treating  
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple  
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal  
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft  
CC rejection, anaemia and septic shock. The fusion proteins are also used in  
CC gene therapy. The present sequence is human TACI-Fc5 variant construct  
CC protein

XX

SQ Sequence 348 AA;

Query Match 76.9%; Score 1263; DB 6; Length 348;

Best Local Similarity 86.7%; Pred. No. 7.9e-84;

Matches 234; Conservative 8; Mismatches 26; Indels 2; Gaps 1;

QY 33 QNEYFDSLHLHACIPQRLCSSNTPPLTCQRYCNASVTNSVKGVDKTHTCPPCPAPELLGG 92

|::| || || | : | : | : | |||||

Db 81 QGKFYDHLRLDCISCASICGQH--PKQCA YFCENKLRSEPKSSDKTHTCPPCPAPEAEGA 138



Qy 93 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 152  
 |||  
 Db 139 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 198  
 Qy 153 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 212  
 |||: |||  
 Db 199 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQVYTLPPSRDE 258  
 Qy 213 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 272  
 |||  
 Db 259 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 318  
 Qy 273 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 302  
 |||  
 Db 319 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 348

RESULT 15

ABJ37102

ID ABJ37102 standard; protein; 608 AA.

XX

AC ABJ37102;

XX

DT 08-MAY-2003 (first entry)

XX

DE Concatameric immunoadhesion human protein sequence SEQ ID No 10.

XX

KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;  
 KW antiarthritic; immunomodulator; concatameric protein; soluble domain;  
 KW dimeric protein; inflammation; septicemia; cytotoxicity;  
 KW rheumatoid arthritis; cachexia; inflammation; human.

XX

OS Homo sapiens.

XX

PN WO2003010202-A1.

XX

PD 06-FEB-2003.

XX

PF 26-JUL-2002; 2002WO-KR001427.

XX

PR 26-JUL-2001; 2001KR-00045028.

XX

PA (MEDE-) MEDEXGEN CO LTD.

XX

PI Chung Y, Han J, Lee H, Choi E, Kim J;

XX

DR WPI; 2003-229639/22.

DR N-PSDB; ABT32045.

XX

PT New concatameric protein having two soluble domains, useful for  
 PT diagnosing and treating disorders associated with the dimeric protein or  
 PT its glycosylated form, such as inflammation, septicemia, rheumatoid  
 PT arthritis and cachexia.

XX

PS Claim 27; Page 139-142; 211pp; English.

XX



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:19:08 ; Search time 20.5062 Seconds  
 (without alignments)  
 760.310 Million cell updates/sec

Title: PCT-US03-05147-3  
 Perfect score: 1643  
 Sequence: 1 METDTLLLWVLLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result |     |        | %     |        |    |                   | Description       |
|--------|-----|--------|-------|--------|----|-------------------|-------------------|
|        | No. | Score  | Match | Length | ID |                   |                   |
|        | 1   | 1264.5 | 77.0  | 398    | 4  | US-09-612-033B-14 | Sequence 14, Appl |
|        | 2   | 1257.5 | 76.5  | 360    | 4  | US-09-180-100-11  | Sequence 11, Appl |
|        | 3   | 1257.5 | 76.5  | 376    | 4  | US-09-180-100-22  | Sequence 22, Appl |
|        | 4   | 1250.5 | 76.1  | 387    | 1  | US-08-470-299-4   | Sequence 4, Appli |
|        | 5   | 1243   | 75.7  | 371    | 1  | US-08-236-311-7   | Sequence 7, Appli |
|        | 6   | 1243   | 75.7  | 371    | 3  | US-08-457-918-7   | Sequence 7, Appli |
|        | 7   | 1243   | 75.7  | 446    | 3  | US-08-397-411-7   | Sequence 7, Appli |
|        | 8   | 1243   | 75.7  | 449    | 1  | US-08-458-516-13  | Sequence 13, Appl |
|        | 9   | 1243   | 75.7  | 459    | 1  | US-08-157-101A-7  | Sequence 7, Appli |
|        | 10  | 1243   | 75.7  | 476    | 2  | US-08-378-939-10  | Sequence 10, Appl |
|        | 11  | 1243   | 75.7  | 547    | 4  | US-09-746-359A-54 | Sequence 54, Appl |

|    |        |      |     |   |                   |                   |
|----|--------|------|-----|---|-------------------|-------------------|
| 12 | 1243   | 75.7 | 571 | 4 | US-09-746-359A-53 | Sequence 53, Appl |
| 13 | 1243   | 75.7 | 951 | 4 | US-09-313-942-9   | Sequence 9, Appli |
| 14 | 1241   | 75.5 | 331 | 3 | US-09-178-869-2   | Sequence 2, Appli |
| 15 | 1241   | 75.5 | 331 | 4 | US-09-761-413-2   | Sequence 2, Appli |
| 16 | 1240   | 75.5 | 482 | 4 | US-09-189-129-2   | Sequence 2, Appli |
| 17 | 1239.5 | 75.4 | 347 | 1 | US-07-940-861-43  | Sequence 43, Appl |
| 18 | 1239.5 | 75.4 | 347 | 1 | US-08-459-512-43  | Sequence 43, Appl |
| 19 | 1239.5 | 75.4 | 347 | 2 | US-08-459-657-43  | Sequence 43, Appl |
| 20 | 1239.5 | 75.4 | 347 | 2 | US-08-460-132-43  | Sequence 43, Appl |
| 21 | 1239.5 | 75.4 | 347 | 3 | US-08-466-465-8   | Sequence 8, Appli |
| 22 | 1239.5 | 75.4 | 347 | 5 | PCT-US92-02050-43 | Sequence 43, Appl |
| 23 | 1239   | 75.4 | 462 | 4 | US-09-289-942A-7  | Sequence 7, Appli |
| 24 | 1239   | 75.4 | 475 | 4 | US-09-740-002-27  | Sequence 27, Appl |
| 25 | 1239   | 75.4 | 476 | 3 | US-08-487-550-4   | Sequence 4, Appli |
| 26 | 1239   | 75.4 | 476 | 3 | US-08-487-550-12  | Sequence 12, Appl |
| 27 | 1239   | 75.4 | 476 | 4 | US-09-526-098-4   | Sequence 4, Appli |
| 28 | 1239   | 75.4 | 476 | 4 | US-09-526-098-12  | Sequence 12, Appl |
| 29 | 1239   | 75.4 | 478 | 3 | US-08-487-550-8   | Sequence 8, Appli |
| 30 | 1239   | 75.4 | 478 | 4 | US-09-526-098-8   | Sequence 8, Appli |
| 31 | 1238.5 | 75.4 | 592 | 4 | US-09-313-942-8   | Sequence 8, Appli |
| 32 | 1238   | 75.3 | 424 | 4 | US-09-333-593A-8  | Sequence 8, Appli |
| 33 | 1238   | 75.3 | 446 | 4 | US-09-157-452B-12 | Sequence 12, Appl |
| 34 | 1238   | 75.3 | 488 | 3 | US-08-776-511-2   | Sequence 2, Appli |
| 35 | 1237   | 75.3 | 229 | 4 | US-09-122-144-2   | Sequence 2, Appli |
| 36 | 1237   | 75.3 | 232 | 2 | US-08-595-043A-50 | Sequence 50, Appl |
| 37 | 1237   | 75.3 | 330 | 4 | US-09-301-593-22  | Sequence 22, Appl |
| 38 | 1237   | 75.3 | 396 | 2 | US-08-784-512-3   | Sequence 3, Appli |
| 39 | 1237   | 75.3 | 396 | 3 | US-09-176-228-3   | Sequence 3, Appli |
| 40 | 1237   | 75.3 | 424 | 5 | PCT-US95-03866-12 | Sequence 12, Appl |
| 41 | 1237   | 75.3 | 424 | 5 | PCT-US95-03866-14 | Sequence 14, Appl |
| 42 | 1237   | 75.3 | 437 | 5 | PCT-US96-10043-11 | Sequence 11, Appl |
| 43 | 1237   | 75.3 | 442 | 4 | US-08-472-888A-7  | Sequence 7, Appli |
| 44 | 1237   | 75.3 | 442 | 5 | PCT-US96-10043-9  | Sequence 9, Appli |
| 45 | 1237   | 75.3 | 451 | 2 | US-08-887-352B-14 | Sequence 14, Appl |

#### ALIGNMENTS

##### RESULT 1

US-09-612-033B-14

; Sequence 14, Application US/09612033B

; Patent No. 6627199

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: Isolation, Identification, and Characterization of

; TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily

; TITLE OF INVENTION: of Genes

; FILE REFERENCE: 01017/35434A

; CURRENT APPLICATION NUMBER: US/09/612,033B

; CURRENT FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

```

;   LENGTH: 398
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
;   OTHER INFORMATION: consisting of Mus musculus sequences and
;   OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

```

## RESULT 2

```

US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-11

```

Query Match 76.5%; Score 1257.5; DB 4; Length 360;  
Best Local Similarity 84.8%; Pred. No. 6e-112;

[illegible]

Query Match 76.5%; Score 1257.5; DB 4; Length 376;  
Best Local Similarity 84.8%; Pred. No. 6.3e-112;  
Matches 240; Conservative 8; Mismatches 20; Indels 15; Gaps 4;

|    |     |  |     |
|----|-----|--|-----|
| Db | 214 | HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR | 273 |
| Qy | 200 | EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF | 259 |
| Db | 274 | EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF | 333 |
| Qy | 260 | FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK                  | 302 |
| Db | 334 | FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK                  | 376 |

RESULT 4

US-08-470-299-4

; Sequence 4, Application US/08470299

; Patent No. 5783181

; GENERAL INFORMATION:

; APPLICANT: Browne, Michael J.

; APPLICANT: Murphy, Kay E.

; APPLICANT: Chapman, Conrad G.

; APPLICANT: Clinkenbeard, Helen E.

; APPLICANT: Young, Peter R.

; APPLICANT: Shatzman, Allan R.

; TITLE OF INVENTION: No. 5783181el Compounds

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road, P.O. Box 1539

; CITY: King of Prussia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,299

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; REFERENCE/DOCKET NUMBER: P31005C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5024

; TELEFAX: 610-270-5090

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 387 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-470-299-4

Query Match

76.1%; Score 1250.5; DB 1; Length 387;

Best Local Similarity 92.1%; Pred. No. 3.1e-111;  
Matches 233; Conservative 1; Mismatches 4; Indels 15; Gaps 1;

[illegible]

## RESULT 5

US-08-236-311-7

; Sequence 7, Application US/08236311

; Patent No. 5565335

; GENERAL INFORMATION:

; APPLICANT: Capon, Daniel J.

APPLICANT: Gregory, Timothy J.

TITLE OF INVENTION: Adhesion Variants

; NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

```
; STATE: California
```

COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
```

; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM:  PC-DOS/MS-DOS

```

; SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/236,311

; FILING DATE: 02-MAY-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/936190

FILING DATE: 26-AUG-1992

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/842777

FILING DATE: 18-FEB-1992

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/250785







QY 229 PSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 288  
 |||||  
 Db 298 PSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 357  
 QY 289 NHYTQKSLSLSPGK 302  
 |||||  
 Db 358 NHYTQKSLSLSPGK 371

RESULT 7

US-08-397-411-7

; Sequence 7, Application US/08397411

; Patent No. 6129914

; GENERAL INFORMATION:

; APPLICANT: Weiner, George

; APPLICANT: Gingrich, Roger

; APPLICANT: Link, Brian

; APPLICANT: Tso, J. Yun

; TITLE OF INVENTION: Bispecific Antibody Effective to Treat

; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/397,411

; FILING DATE: 01-MAR-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/859,583

; FILING DATE: 27-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 011823-004901

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 446 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-397-411-7

Query Match 75.7%; Score 1243; DB 3; Length 446;  
Best Local Similarity 92.1%; Pred. No. 2e-110;  
Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 51  | CSSNTPPLTCQRYCNASVTNSV--KGVDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI | 108 |
| Db | 199 | CNVNHKP-----SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI   | 252 |
| Qy | 109 | SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW  | 168 |
| Db | 253 | SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW  | 312 |
| Qy | 169 | LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY  | 228 |
| Db | 313 | LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY  | 372 |
| Qy | 229 | PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH  | 288 |
| Db | 373 | PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH  | 432 |
| Qy | 289 | NHYTQKSLSLSPGK  | 302 |
| Db | 433 | NHYTQKSLSLSPGK  | 446 |

## RESULT 8

US-08-458-516-13

; Sequence 13, Application US/08458516

; Patent No. 5777085

; GENERAL INFORMATION:

APPLICANT: Co, Man Sung

APPLICANT: Tso, J. Yun

10; TITLE OF INVENTION: Humanized Antibodies Reactive with

10 TITLE OF INVENTION: GPIIB/IIIA

```

; NUMBER OF SEQUENCES: 23

```

CORRESPONDENCE ADDRESS:

: ADDRESSEE: William M. Smith

```

; STREET:  One Market Plaza, Steuart Tower, Suite 2000

```

CITY: San Francisco

; STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS

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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/458,516

FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/059,159

; FILING DATE: 03-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223







```

Qy      289 NHYTQKSLSLSPGK 302
          |||||
Db      463 NHYTQKSLSLSPGK 476

```

```

RESULT 11
US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-54

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Query Match 75.7%; Score 1243; DB 4; Length 547;  
Best Local Similarity 92.1%; Pred. No. 2.7e-110;  
Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

[illegible]



Qy 289 NHYTQKSLSLSPGK 302  
 |||||  
 Db 534 NHYTQKSLSLSPGK 547

```

RESULT 12
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 53
;   LENGTH: 571
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-53

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Query Match 75.7%; Score 1243; DB 4; Length 571;  
Best Local Similarity 92.1%; Pred. No. 2.8e-110;  
Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 51  | CSSNTPPLTCQRYCNASVTNSV---KGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI | 108 |
| Db | 324 | CNVNHKP-----SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI   | 377 |
| Qy | 109 | SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW  | 168 |
| Db | 378 | SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW  | 437 |
| Qy | 169 | LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY  | 228 |
| Db | 438 | LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY  | 497 |
| Qy | 229 | PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALH   | 288 |
| Db | 498 | PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALH   | 557 |

Qy 289 NHYTQKSLSLSPGK 302  
 |||||  
 Db 558 NHYTQKSLSLSPGK 571

### RESULT 13

US-09-313-942-9

```
; Sequence 9, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
;   APPLICANT: REGENERON PHARMACEUTICALS, INC.
;   TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
;   TITLE OF INVENTION:   AND USING
;   FILE REFERENCE: REG 203-A
;   CURRENT APPLICATION NUMBER: US/09/313,942
;   CURRENT FILING DATE:   1999-05-19
;   PRIOR APPLICATION NUMBER: 09/313,942
;   PRIOR FILING DATE: 1999-05-19
;   PRIOR APPLICATION NUMBER: 60/101,858
;   PRIOR FILING DATE: 1998-09-25
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 951
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-313-942-9
```

Query Match 75.7%; Score 1243; DB 4; Length 951;  
Best Local Similarity 92.1%; Pred. No. 6e-110;  
Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 51  | CSSNTPPLTCQRYCNASVTNSV--KGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI | 108 |
| Db | 704 | CNVNHKP-----SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  | 757 |
| Qy | 109 | SRTPEVTCVWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW | 168 |
| Db | 758 | SRTPEVTCVWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW | 817 |
| Qy | 169 | LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY | 228 |
| Db | 818 | LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY | 877 |
| Qy | 229 | PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH | 288 |
| Db | 878 | PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH | 937 |
| Qy | 289 | NHYTQKSLSLSPGK   | 302 |
| Db | 938 | NHYTOKSLSLSPGK   | 951 |

RESULT 14

US-09-178-869-2

; Sequence 2, Application US/09178869B

```
; Patent No. 6197294
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/178,869B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2
```

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Query Match          75.5%; Score 1241; DB 3; Length 331;
Best Local Similarity 78.7%; Pred. No. 2e-110;
Matches 240; Conservative 9; Mismatches 30; Indels 26; Gaps 3;
```

```
Qy      20 GDVTMLQ MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQ----- 61
      || : ::| : | |: | : || : |
Db      31 GDN SHVEMKLA VDEEENADNNTKANVT KPKRCSGS----IC YGTIAVIVFFLIGFMIGYL 86

Qy      62 RYCNA----SVTNSVKGV DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 117
      || : : | | |||||
Db      87 GYCKGVEPKTEGSEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 146

Qy     118 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 177
      |||||
Db     147 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 206

Qy     178 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 237
      |||||
Db     207 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 266

Qy     238 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLS 297
      |||||
Db     267 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLS 326

Qy     298 LSPGK 302
      |||||
Db     327 LSPGK 331
```

# RESULT 15

```
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hammang, Joseph P.
```

```
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/761,413
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/178,869
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-413-2
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Query Match          75.5%; Score 1241; DB 4; Length 331;
Best Local Similarity 78.7%; Pred. No. 2e-110;
Matches 240; Conservative 9; Mismatches 30; Indels 26; Gaps 3;
```

```
Qy      20 GDVTMLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ----- 61
      || : ::| : | | : | | : || : |
Db      31 GDNSHVEMLAVDEEENADNNTKANVTKPKRCSGS----ICYGTIIVIVFFLIGFMIGYL 86

Qy      62 RYCNA----SVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 117
      || : : | | |||||
Db      87 GYCKGVEPKTEGSEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 146

Qy     118 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 177
      |||||
Db     147 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 206

Qy     178 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 237
      |||||
Db     207 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 266

Qy     238 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS 297
      |||||
Db     267 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS 326

Qy     298 LSPGK 302
      ||||
Db     327 LSPGK 331
```

```
Search completed: April 19, 2004, 13:24:21
Job time : 21.5062 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:18:32 ; Search time 16.7778 Seconds  
(without alignments)  
1731.447 Million cell updates/sec

Title: PCT-US03-05147-3  
Perfect score: 1643  
Sequence: 1 METDTLLLWVLLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | % Query |        | DB | ID     | Description        |
|------------|--------|---------|--------|----|--------|--------------------|
|            |        | Match   | Length |    |        |                    |
| 1          | 1243   | 75.7    | 330    | 1  | GHU    | Ig gamma-1 chain C |
| 2          | 1237.5 | 75.3    | 374    | 2  | S69339 | Ig heavy chain V r |
| 3          | 1237   | 75.3    | 255    | 4  | S31866 | Ig gamma-1 chain C |
| 4          | 1186   | 72.2    | 234    | 2  | PT0207 | Ig gamma chain C r |
| 5          | 1163   | 70.8    | 377    | 2  | A23511 | Ig gamma-3 chain C |
| 6          | 1161   | 70.7    | 377    | 2  | A60764 | Ig gamma-3 chain C |
| 7          | 1153   | 70.2    | 326    | 1  | G2HU   | Ig gamma-2 chain C |
| 8          | 1142   | 69.5    | 327    | 1  | G4HU   | Ig gamma-4 chain C |
| 9          | 1138.5 | 69.3    | 289    | 1  | G3HUWI | Ig gamma-3 heavy c |
| 10         | 934.5  | 56.9    | 323    | 1  | GHRB   | Ig gamma chain C r |
| 11         | 918.5  | 55.9    | 328    | 2  | I47159 | Ig gamma 2a chain  |
| 12         | 917    | 55.8    | 328    | 2  | I47160 | Ig gamma 2b chain  |
| 13         | 915    | 55.7    | 277    | 2  | I47162 | Ig gamma 4 chain c |

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 14 | 903.5 | 55.0 | 329 | 1 | G2GP   | Ig gamma-2 chain C |
| 15 | 898.5 | 54.7 | 328 | 2 | I47158 | Ig gamma 1 chain c |
| 16 | 891.5 | 54.3 | 328 | 2 | I47161 | Ig gamma 3 chain c |
| 17 | 870.5 | 53.0 | 470 | 2 | S22080 | Ig heavy chain pre |
| 18 | 856   | 52.1 | 329 | 1 | G3MSC  | Ig gamma-3 chain C |
| 19 | 854   | 52.0 | 308 | 2 | C30554 | Ig heavy chain C r |
| 20 | 854   | 52.0 | 472 | 2 | S31459 | Ig gamma-1 chain - |
| 21 | 849   | 51.7 | 333 | 2 | PS0018 | Ig gamma-2b chain  |
| 22 | 845   | 51.4 | 398 | 1 | G3MSM  | Ig gamma-3 chain C |
| 23 | 836.5 | 50.9 | 444 | 2 | PC4436 | monoclonal antibod |
| 24 | 827   | 50.3 | 326 | 2 | PS0017 | Ig gamma-1 chain C |
| 25 | 826   | 50.3 | 329 | 2 | S00847 | Ig gamma-2c chain  |
| 26 | 825.5 | 50.2 | 324 | 1 | G1MS   | Ig gamma-1 chain C |
| 27 | 820.5 | 49.9 | 393 | 1 | G1MSM  | Ig gamma-1 chain C |
| 28 | 819.5 | 49.9 | 330 | 1 | G2MSA  | Ig gamma-2a chain  |
| 29 | 819.5 | 49.9 | 469 | 2 | S37483 | Ig gamma-2a chain  |
| 30 | 818.5 | 49.8 | 335 | 1 | G2MSAB | Ig gamma-2a chain  |
| 31 | 814.5 | 49.6 | 399 | 1 | G2MSAM | Ig gamma-2a chain  |
| 32 | 804.5 | 49.0 | 446 | 2 | S40295 | Ig gamma-2a chain  |
| 33 | 796   | 48.4 | 322 | 2 | PS0019 | Ig gamma-2a chain  |
| 34 | 792   | 48.2 | 474 | 1 | G2MS11 | Ig gamma-2b chain  |
| 35 | 785   | 47.8 | 327 | 2 | S06611 | Ig gamma-2 chain C |
| 36 | 784.5 | 47.7 | 405 | 1 | G2MSBM | Ig gamma-2b chain  |
| 37 | 767.5 | 46.7 | 475 | 2 | S01321 | Ig gamma-2b chain  |
| 38 | 707   | 43.0 | 180 | 2 | I46732 | Ig gamma heavy cha |
| 39 | 577.5 | 35.1 | 249 | 2 | S69340 | Ig heavy chain VHI |
| 40 | 574.5 | 35.0 | 218 | 2 | A36040 | Ig heavy chain V-I |
| 41 | 571   | 34.8 | 152 | 2 | S14236 | Ig gamma-1 chain C |
| 42 | 400   | 24.3 | 572 | 2 | B46529 | Ig Y heavy chain ( |
| 43 | 364.5 | 22.2 | 549 | 2 | S04845 | Ig heavy chain pre |
| 44 | 362.5 | 22.1 | 388 | 1 | EHMS   | Ig epsilon chain C |
| 45 | 359.5 | 21.9 | 548 | 2 | S38864 | Ig epsilon chain C |

#### ALIGNMENTS

##### RESULT 1

GHHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999

C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, 239-Asp and 241-Leu

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861  
 A;Molecule type: DNA  
 A;Residues: 2-330 <HAR>  
 A;Cross-references: EMBL:Z17370  
 R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
 Cell 29, 671-679, 1982  
 A;Title: Structure of human immunoglobulin gamma genes: implications for  
 evolution of a gene family.  
 A;Reference number: S33887; MUID:83001943; PMID:6811139  
 A;Accession: S33887  
 A;Molecule type: DNA  
 A;Residues: 88-113;235-330 <TAK>  
 A;Cross-references: EMBL:Z17370  
 R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.;  
 Edelman, G.M.  
 Biochemistry 9, 3161-3170, 1970  
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino  
 acid sequence of heavy-chain cyanogen bromide fragments H-1-H-4.  
 A;Reference number: A90563; MUID:71064024; PMID:5489771  
 A;Contents: myeloma protein Eu  
 A;Accession: B90563  
 A;Molecule type: protein  
 A;Residues: 1-96,'R',98-135 <CUN>  
 A;Note: this sequence has the Glm(3) marker, 97-Arg  
 R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman,  
 G.M.  
 Biochemistry 9, 3171-3181, 1970  
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino  
 acid sequence of heavy-chain cyanogen bromide fragments H-5-H-7.  
 A;Reference number: A90564; MUID:71064025; PMID:5530842  
 A;Contents: Eu  
 A;Accession: A90564  
 A;Molecule type: protein  
 A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-  
 238,'E',240,'M',242-267,'DGEPE',273-329 <RUT>  
 A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met  
 R;Ponstingl, H.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
 A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins  
 (Myelomprotein Nie), III. Die chymotryptischen Peptide der H-Kette, Anordnung  
 der tryptischen Peptide und Diskussion der vollstaendigen Primaerstruktur.  
 A;Reference number: A91668; MUID:77070269; PMID:826475  
 A;Contents: myeloma protein Nie  
 A;Accession: B91668  
 A;Molecule type: protein  
 A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-  
 268,'E',270-271,'D',273-330 <PON>  
 A;Note: this sequence has the Glm(17) and Glm(1) markers  
 R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
 A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins  
 IgG1 KOL, I.  
 A;Reference number: A91723; MUID:83289131; PMID:6884994  
 A;Contents: myeloma protein KOL; disulfide bonds  
 A;Accession: A91723  
 A;Molecule type: protein





|||||  
Db 317 NHYTQKSLSLSPGK 330

RESULT 2

S69339

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000

C;Accession: S69339; S72664

R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A;Reference number: S69339; MUID:95262687; PMID:7744049

A;Accession: S69339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <KHA>

A;Cross-references: EMBL:X81695

R;Khamlichi, A.A.

submitted to the EMBL Data Library, September 1994

A;Reference number: S72664

A;Accession: S72664

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140,'C',142-374 <KH2>

A;Cross-references: EMBL:X81695

C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 75.3%; Score 1237.5; DB 2; Length 374;  
Best Local Similarity 79.0%; Pred. No. 2.5e-82;  
Matches 237; Conservative 9; Mismatches 23; Indels 31; Gaps 2;

```
Qy      23 TMLQMAGQCSQNEYFDSLHACIPQQLRCSSNTPPLTCQRYCNAS----- 67
      | | : | : | | | | | | | | | | | | | | | | | | | | | | |
Db      86 TRLTITKDTSKNQVV-----LTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQ 134

Qy      68 -----VTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 122
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     135 GTLVTVSSEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 194

Qy     123 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 182
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     195 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 254

Qy     183 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 242
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     255 LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP 314

Qy     243 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 302
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     315 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 374
```

RESULT 3

S31866



Best Local Similarity 94.8%; Pred. No. 7.8e-79;  
Matches 221; Conservative 1; Mismatches 9; Indels 2; Gaps 1;

[illegible]

## RESULT 5

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 23-Jul-1999

C;Accession: A23511

R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A7>Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region  
gene: comparison with the other human C-gamma genes.

A;Reference number: A23511; MUJID:86148507; PMID:3081877

A;Accession: A23511

A;Molecule type: DNA

A;Residues: 1-377 &lt;HUC&gt;

A;Cross-references: GB:X03604; GB:M12958; NID:q33070; PIDN:CAA27268.1;

PID:q577056

C; Genetics:

A; Gene: GDB:IGHG3

A;Cross-references: GDB:119339; OMIM:147120

```
A;Map position: 14q32.33-14q32.33
```

A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C; Superfamily: immunoglobulin C region; immunoglobulin homology

C; Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 1163; DB 2; Length 377;  
Best Local Similarity 84.7%; Pred. No. 6.4e-77;  
Matches 221; Conservative 9; Mismatches 19; Indels 12; Gaps 4;

|      |     |  |     |
|------|-----|--|-----|
| Qy   | 46  | PCQLRC----SSNTPLTCQRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPK  | 101 |
|      |     | :  |     |
| Db   | 125 | PCP-RCPEPKSCDTPP-PCR-----CPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPK   | 176 |
| <br> |     |  |     |
| Qy   | 102 | PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL | 161 |
|      |     | :                             :                              |     |
| Db   | 177 | PKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVL | 236 |



RESULT 7

G2HU

Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 <ELL>

A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056

A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.

A;Reference number: A92809; MUID:81007873; PMID:6774012

A;Contents: myeloma protein Til

A;Accession: A92809

A;Molecule type: protein

A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>

A;Note: Trp-156 is at or near the complement-binding site

R;Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A;Title: The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.

A;Reference number: A90752; MUID:80001357; PMID:113060

A;Contents: myeloma protein Zie

A;Accession: A90752

A;Molecule type: protein

A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-234,'Z',236-263,'BGEPEZ',269-325 <CON>

A;Note: this sequence has since been revised

R;Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.

A;Reference number: A93132; MUID:80114419; PMID:118920

A;Contents: Zie

A;Accession: A93132

A;Molecule type: protein

A;Residues: 238-275 <HOF>

R;Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A;Reference number: A94591

A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidation states of residues 58, 194, and 197; the amidation states of residues 172-174, 176, and 235 were not determined

R;Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A;Reference number: A90253; MUID:72033500; PMID:4940472  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969

Query Match 70.2%; Score 1153; DB 1; Length 326;  
Best Local Similarity 87.6%; Pred. No. 2.8e-76;  
Matches 218; Conservative 8; Mismatches 15; Indels 8; Gaps 3;

RESULT 8



||||||| ||  
Db 315 HYTQKSLSLSLGK 327

RESULT 9

G3HUWI

Ig gamma-3 heavy chain disease proteins - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #text\_change 16-Jul-1999

C;Accession: A90442; A92219; A90198; A93915; A02149

R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein Wis.

A;Reference number: A90442; MUID:81021548; PMID:6774747

A;Contents: heavy chain disease protein Wis

A;Accession: A90442

A;Molecule type: protein

A;Residues: 1-289 <FRA>

A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain disulfide bond at position 7 in addition to the 11 normally present in the hinge region

A;Note: this protein lacks most of the V region and all of the CH1 region.

Residue 12 corresponds to the beginning of the hinge region of normal gamma-3 chains

A;Note: the sequence of residues 42-76 was taken from the reference that follows

R;Michaelson, T.E.; Frangione, B.; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977

A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.

A;Reference number: A92219; MUID:77118561; PMID:402363

A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein Wis

A;Accession: A92219

A;Molecule type: protein

A;Residues: 12-97 <MIC>

A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma chains and contains three identical 15-residue segments (29-43, 44-58, and 59-73) preceded by a similar 17-residue segment (12-28)

A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter-heavy chain bonds

R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.

Biochem. Biophys. Res. Commun. 71, 907-914, 1976

A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the Fc fragment of immunoglobulin G3.

A;Reference number: A90198; MUID:77021516; PMID:823945

A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues 59-289 of protein Wis

A;Accession: A90198

A;Molecule type: protein

A;Residues: 59-125,'EB',128-226,228-289 <WOL>

A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the hinge compared with normal gamma-3 heavy chains

R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Buxbaum, J.N.

Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982





A;Reference number: A91749; MUID:84030930; PMID:6313520  
 A;Accession: A91749  
 A;Molecule type: mRNA  
 A;Residues: 1-323 <BER>  
 A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
 R;Pratt, D.M.; Mole, L.E.  
 Biochem. J. 151, 337-349, 1975  
 A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.  
 A;Reference number: A90290; MUID:76135469; PMID:1243651  
 A;Accession: A90290  
 A;Molecule type: protein  
 A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>  
 R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
 A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain and identification of two genomic C-gamma genes.  
 A;Reference number: A93928; MUID:83299917; PMID:6193512  
 A;Accession: A93928  
 A;Molecule type: mRNA  
 A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>  
 A;Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112  
 A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker, 185-Ala  
 R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
 Biochem. J. 116, 249-259, 1970  
 A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.  
 A;Reference number: A90245; MUID:70110015; PMID:5461106  
 A;Accession: A90245  
 A;Molecule type: protein  
 A;Residues: 132-143,'E',145-161 <FRU>  
 R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.  
 in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, Stockholm, 1967  
 A;Reference number: A94416  
 A;Accession: A94416  
 A;Molecule type: protein  
 A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',234-245,'D',247-255,'G',257-259,'D',261-265,'D',267-279,'W',281-283,'S',285-322 <HIL>  
 A;Note: this has the e15 allotypic marker, 185-Ala  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;20-82/Domain: immunoglobulin homology <IM1>  
 F;130-199/Domain: immunoglobulin homology <IM2>  
 F;236-303/Domain: immunoglobulin homology <IM3>  
 F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 934.5; DB 1; Length 323;  
 Best Local Similarity 68.0%; Pred. No. 1.9e-60;  
 Matches 174; Conservative 33; Mismatches 40; Indels 9; Gaps 3;

[illegible]

Db 150 PEVQFSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPA 209

Qy 186 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PE 243  
 || : ||||| ||||| :||::||:| || || ||: || ||

Db 210 PITRIISKAKGQTREPQVYTLPPHAEELSRKVSITCLVIGFYPPDIDVEWQRNGQPEPE 269

Qy 244 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302  
 ||:|||| | ||:|||| :||: || | :| :|||||||:| :||

Db 270 GNYRTTPPQQDVGTYFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

# RESULT 12

I47160

Ig gamma 2b chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C;Accession: I47160

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single animal.

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47160

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-328 <KAC>

A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126

C;Genetics:

A;Gene: IgG2b

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 55.8%; Score 917; DB 2; Length 328;

Best Local Similarity 66.9%; Pred. No. 3.6e-59;

Matches 172; Conservative 34; Mismatches 35; Indels 16; Gaps 5;

Qy 58 LTCQRY-CNASVTNSVKGVDK---THTCPPCP-----APELLGGPSVFLFPPKPKDTLM 107  
 | : | | : : || | | | :| ||||:|||||

Db 76 LSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----GPSVFIFPPKPKDTLM 131

Qy 108 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD 167  
 ||||:||||| |::||:|:||||| |::|:|:|:||||| : ||

Db 132 ISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQD 191

Qy 168 WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF 227  
 ||||:||||:| |||| : ||||| ||||| :||::||:| || ||

Db 192 WLNGKEFKCKVNNKDLPAITRIISKAKGQTREPQVYTLPPHAEELSRKVSITCLVIGF 251

Qy 228 YPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 285  
 || || ||: || || ||:| || | ||::||| :||: || | :| |||

Db 252 YPPDIDVEWQRNGQPEPEGNYRTTPPQQDVGTYFLYSKFSVDKASWQGGGIFQCAVMHE 311

Qy 286 ALHNHYTQKSLSLSPGK 302  
 |||||:| :||

Db 312 ALHNHYTQKSISKTPGK 328

## I47162

C;Species: Sus scrofa domestica (domestic pig)

C;Accession: I47162

J. Immunol. 153, 3565-3573, 1994

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47162

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-277 <KAC>

A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130

## C; Genetics:

A; Gene: IqG4

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;82-151/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 915; DB 2; Length 277;  
Best Local Similarity 68.0%; Pred. No. 4.1e-59;  
Matches 172; Conservative 33; Mismatches 40; Indels 8; Gaps 5;

```
Qy          58 LTCQRY-CNASVTNSVKGVDK---THTCPPCP-APELLG-GPSVFLFPKPKDTLMISRT 111
           |: : | || :   |||   || |||||   |   ||| : |||||
```

Db 25 LSSKSYTCNVNHPATTTKVDKRVGTTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRT 84

QY            112 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG    171  
               :|:|||||:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 85 PKVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKKEQFNSTYRVVSVLP IOHODWLNG 144

Qy 172 KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD 231  
||:||||:| ||||| : | ||||| ||||| ||||| : ||||| : |||||

Db 145 KEFKCKVNNKDLPAITRIISKAKGQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPD 204

QY            232 IAVEWESNGQ--PENNYKTTTPVLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN    289  
| | | : | | | | : | | | | | : | | | | : | | | |

Db 205 IDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHN 264

Qy 290 HYTQKSLSLSPGK 302  
||| | : : |||

Db 265 HYTQKSIFKTPGK 277

G2GP

Ig gamma-2 chain C region - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 07-May-1981 #sequence revision 07-May-1981 #text change 16-Jul-1999

C;Accession: A94553; A90352; A90359; A90384; A90385; A02151

R;Trischmann, T.M.

submitted to the Atlas, April 1975

A;Reference number: A94553

A;Accession: A94553

A;Molecule type: protein

A;Residues: 1-3 <TRI>  
 R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
 Biochemistry 10, 18-25, 1971  
 A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2).  
 III. Amino acid sequence of the region around the half-cystine joining heavy and  
 light chains.  
 A;Reference number: A90352; MUID:71058471; PMID:5538606  
 A;Accession: A90352  
 A;Molecule type: protein  
 A;Residues: 4-68 <BIR>  
 R;Turner, K.J.; Cebra, J.J.  
 Biochemistry 10, 9-17, 1971  
 A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2).  
 II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen  
 bromide fragments.  
 A;Reference number: A90359; MUID:71058486; PMID:5538616  
 A;Accession: A90359  
 A;Molecule type: protein  
 A;Residues: 69-133;312-329 <TUR>  
 R;Tracey, D.E.; Cebra, J.J.  
 Biochemistry 13, 4796-4803, 1974  
 A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2  
 antibodies.  
 A;Reference number: A90384; MUID:75036072; PMID:4429665  
 A;Accession: A90384  
 A;Molecule type: protein  
 A;Residues: 134-226 <TRA>  
 R;Trischmann, T.M.; Cebra, J.J.  
 Biochemistry 13, 4804-4811, 1974  
 A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2  
 antibodies.  
 A;Reference number: A90385; MUID:75036073; PMID:4609467  
 A;Accession: A90385  
 A;Molecule type: protein  
 A;Residues: 227-311 <TR2>  
 R;Oliveira, B.; Lamm, M.E.  
 Biochemistry 10, 26-31, 1971  
 A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
 A;Reference number: A90354; MUID:71058474; PMID:4922544  
 A;Contents: annotation; disulfide bonds  
 A;Note: Cys-16 is involved in a heavy-light chain bond  
 A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
 C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea  
 pigs.  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical  
 light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma,  
 or mu) chains usually stabilized by interchain disulfide bonds. In some cases,  
 such as IgA and IgM, the subunits associate into larger oligomers.  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;21-81/Domain: immunoglobulin homology <IM1>  
 F;135-204/Domain: immunoglobulin homology <IM2>  
 F;241-310/Domain: immunoglobulin homology <IM3>  
 F;28-79/Disulfide bonds: #status experimental  
 F;142-202/Disulfide bonds: #status experimental  
 F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;248-308/Disulfide bonds: #status experimental

Query Match 55.0%; Score 903.5; DB 1; Length 329;  
 Best Local Similarity 65.8%; Pred. No. 3.4e-58;  
 Matches 171; Conservative 27; Mismatches 49; Indels 13; Gaps 2;

```

Qy      55 TPPLTCQRYCNASVTSVKGVDKT-----HTCPPCPAPELLGGPSVFLFPPKPK 103
      | | : : | | : | ||| || | | |||||:|||||
Db      70 TVPSSQKATCNVAHPASSTKVDKTVEPIRTPZPBPCCTCPKCPPPENLGGPSVFIFFPKPK 129

Qy     104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
      ||||| || ||||| ||| :|||:| |:|| | ||:|||| |||:|:| ||| :
Db     130 DTLMISLTPRVTCVVVDVSQDEPEVQFTWTFVDNKPVGNAETKPRVEQYNTTFRVESVLPI 189

Qy     164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
      ||||| |||:|||| ||||| || || | ||||| ||||:|:| |||
Db     190 QHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPSRDELSKSKVSVTCL 249

Qy     224 VKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCS 281
      : |:|:| || | | | | || | | | : |:|:| ||||| || | | |:|:|
Db     250 IINFFPADIHVEWASNRVPVSEKEYKNTPIEDADGSYFLYSKLTVDKSAWDQGTVYTCS 309

Qy     282 VMHEALHNHYTQKSLSLSPG 301
      ||||| |||:| |||
Db     310 VMHEALHNHVTQKAISRSPG 329
  
```

# RESULT 15

I47158

Ig gamma 1 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C;Accession: I47158

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a single animal.

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47158

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-328 <KAC>

A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122

C;Genetics:

A;Gene: IgG1

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 54.7%; Score 898.5; DB 2; Length 328;  
 Best Local Similarity 59.6%; Pred. No. 7.8e-58;  
 Matches 180; Conservative 39; Mismatches 64; Indels 19; Gaps 7;

```

Qy      10 VLLLVWPGS-TGDV---TMLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYC 64
      | : | |:| | :||:| | : | | :| | :|
Db      37 VTVTWNSGALTSGVHTFPSVLQPSGLYSLSSM-----VTVPAS---SLSSKSYTCNVNH 87

Qy     65 NASVTNSVK--GVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 122
      |:| | |: : ||| || | : ||||:||||| ||||| |||||
  
```

Db 88 PATTTKVDKRVGIHQPTCPICPGCE-VAGPSVFIFPPKPKDTLMISQTPEVTCVWVDVS 146  
 Qy 123 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 182  
 | | | : | | | | | | | | | | : | | : | | : | | | | | | | | : | | | | | : | |  
 Db 147 KEHAEVQFSWYVDGVEVHTAETRPKEEQFNSTYRVVSVLPIQHQQDWLKGKEFKCKVNNVD 206  
 Qy 183 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ- 241  
 | | | | : | | | | | | | | | | : | | : | | : | | | | | | | | | | : | | | | |  
 Db 207 LPAPITRTISKAIGQSREPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQP 266  
 Qy 242 -PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 300  
 | | | | : | | | | | | | | | | | | : | | : | | : | | | | | | | | | | : | | :  
 Db 267 EPENTYRTTPPQQDVGDTFFLYSKLAVDKARWDHGDKFECAMHEALHNHYTQKSISKTK 326  
 Qy 301 GK 302  
 | |  
 Db 327 GK 328

Search completed: April 19, 2004, 13:23:36  
 Job time : 17.7778 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:21:03 ; Search time 47.2263 Seconds  
(without alignments)  
1762.857 Million cell updates/sec

Title: PCT-US03-05147-3  
Perfect score: 1643  
Sequence: 1 METDTLLLWVLLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query |       |        |    |    |             |
|--------|-------|-------|--------|----|----|-------------|
| No.    | Score | Match | Length | DB | ID | Description |

|    |        |       |     |    |                   |                   |
|----|--------|-------|-----|----|-------------------|-------------------|
| 1  | 1643   | 100.0 | 302 | 14 | US-10-115-192-12  | Sequence 12, Appl |
| 2  | 1488.5 | 90.6  | 283 | 9  | US-09-854-864-9   | Sequence 9, Appli |
| 3  | 1488.5 | 90.6  | 283 | 12 | US-09-855-158-9   | Sequence 9, Appli |
| 4  | 1398.5 | 85.1  | 281 | 9  | US-09-854-864-10  | Sequence 10, Appl |
| 5  | 1398.5 | 85.1  | 281 | 12 | US-09-855-158-10  | Sequence 10, Appl |
| 6  | 1379   | 83.9  | 334 | 15 | US-10-258-368-8   | Sequence 8, Appli |
| 7  | 1376   | 83.7  | 366 | 15 | US-10-258-368-6   | Sequence 6, Appli |
| 8  | 1361   | 82.8  | 320 | 12 | US-10-411-037-50  | Sequence 50, Appl |
| 9  | 1361   | 82.8  | 320 | 12 | US-10-411-026-50  | Sequence 50, Appl |
| 10 | 1276.5 | 77.7  | 396 | 14 | US-10-193-616-14  | Sequence 14, Appl |
| 11 | 1271   | 77.4  | 332 | 14 | US-10-152-363A-62 | Sequence 62, Appl |
| 12 | 1269   | 77.2  | 446 | 9  | US-09-792-200B-10 | Sequence 10, Appl |
| 13 | 1265.5 | 77.0  | 465 | 9  | US-09-792-200B-6  | Sequence 6, Appli |
| 14 | 1264.5 | 77.0  | 398 | 15 | US-10-622-407-14  | Sequence 14, Appl |
| 15 | 1264.5 | 77.0  | 404 | 15 | US-10-258-368-15  | Sequence 15, Appl |
| 16 | 1263   | 76.9  | 348 | 14 | US-10-152-363A-54 | Sequence 54, Appl |
| 17 | 1260   | 76.7  | 608 | 14 | US-10-363-427-10  | Sequence 10, Appl |
| 18 | 1259.5 | 76.7  | 397 | 9  | US-09-854-864-18  | Sequence 18, Appl |
| 19 | 1259.5 | 76.7  | 397 | 12 | US-09-855-158-18  | Sequence 18, Appl |
| 20 | 1259   | 76.6  | 480 | 14 | US-10-077-023-133 | Sequence 133, App |
| 21 | 1259   | 76.6  | 480 | 14 | US-10-077-023-135 | Sequence 135, App |
| 22 | 1259   | 76.6  | 698 | 9  | US-09-875-338-9   | Sequence 9, Appli |
| 23 | 1259   | 76.6  | 698 | 14 | US-10-077-023-9   | Sequence 9, Appli |
| 24 | 1258   | 76.6  | 344 | 14 | US-10-152-363A-52 | Sequence 52, Appl |
| 25 | 1257.5 | 76.5  | 360 | 9  | US-09-949-713-11  | Sequence 11, Appl |
| 26 | 1257.5 | 76.5  | 376 | 9  | US-09-949-713-22  | Sequence 22, Appl |
| 27 | 1257.5 | 76.5  | 376 | 14 | US-10-084-139-10  | Sequence 10, Appl |
| 28 | 1254   | 76.3  | 266 | 15 | US-10-390-566-21  | Sequence 21, Appl |
| 29 | 1254   | 76.3  | 266 | 15 | US-10-390-566-28  | Sequence 28, Appl |
| 30 | 1254   | 76.3  | 494 | 9  | US-09-792-200B-2  | Sequence 2, Appli |
| 31 | 1253.5 | 76.3  | 357 | 14 | US-10-152-363A-56 | Sequence 56, Appl |
| 32 | 1252   | 76.2  | 266 | 15 | US-10-390-566-8   | Sequence 8, Appli |
| 33 | 1252   | 76.2  | 266 | 15 | US-10-390-566-15  | Sequence 15, Appl |
| 34 | 1252   | 76.2  | 444 | 14 | US-10-363-427-2   | Sequence 2, Appli |
| 35 | 1252   | 76.2  | 628 | 14 | US-10-363-427-6   | Sequence 6, Appli |
| 36 | 1251.5 | 76.2  | 523 | 9  | US-09-792-200B-14 | Sequence 14, Appl |
| 37 | 1251   | 76.1  | 400 | 10 | US-09-389-782-5   | Sequence 5, Appli |
| 38 | 1250.5 | 76.1  | 387 | 12 | US-10-050-227-4   | Sequence 4, Appli |
| 39 | 1249   | 76.0  | 252 | 14 | US-10-145-206-121 | Sequence 121, App |
| 40 | 1249   | 76.0  | 528 | 9  | US-09-792-200B-22 | Sequence 22, Appl |
| 41 | 1248.5 | 76.0  | 535 | 12 | US-10-633-202-3   | Sequence 3, Appli |
| 42 | 1248   | 76.0  | 288 | 10 | US-09-822-851B-14 | Sequence 14, Appl |
| 43 | 1248   | 76.0  | 288 | 14 | US-10-119-637A-14 | Sequence 14, Appl |
| 44 | 1248   | 76.0  | 358 | 14 | US-10-233-150-5   | Sequence 5, Appli |
| 45 | 1247   | 75.9  | 380 | 9  | US-09-948-018-36  | Sequence 36, Appl |

#### ALIGNMENTS

RESULT 1  
 US-10-115-192-12  
 ; Sequence 12, Application US/10115192  
 ; Publication No. US20030082175A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Apotech R & D S.A.

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; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12
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Query Match          100.0%; Score 1643; DB 14; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.3e-125;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 METDTLLLWVLLLWVPGSTGDVTMLQMAGQCSQNEYFDSLLHACIPCQLRCSNTPPLTC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 METDTLLLWVLLLWVPGSTGDVTMLQMAGQCSQNEYFDSLLHACIPCQLRCSNTPPLTC 60

Qy     61 QRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 120

Qy    121 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 180

Qy    181 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 240

Qy    241 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 300

Qy     301 GK 302
        ||
Db     301 GK 302
```

RESULT 2

US-09-854-864-9

```
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA,
```

```
; TITLE OF INVENTION:  BLYS/AGP-3, AND TACI
; FILE REFERENCE:  A-686B
; CURRENT APPLICATION NUMBER:  US/09/854,864
; CURRENT FILING DATE:  2001-09-11
; PRIOR APPLICATION NUMBER:  US 60/204,039
; PRIOR FILING DATE:  2000-05-12
; PRIOR APPLICATION NUMBER:  US 60/214,591
; PRIOR FILING DATE:  2000-06-27
; NUMBER OF SEQ ID NOS:  31
; SOFTWARE:  PatentIn version 3.1
; SEQ ID NO 9
; LENGTH:  283
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-854-864-9
```

```
Query Match          90.6%;  Score 1488.5;  DB 9;  Length 283;
Best Local Similarity  97.2%;  Pred. No. 4.6e-113;
Matches  275;  Conservative  0;  Mismatches  1;  Indels  7;  Gaps  1;
```

```
Qy      27  MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGV-----DKTH 79
          |||
Db      1  MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTNAGGGGGDKTH 60

Qy      80  TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 139
          |||
Db      61  TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 120

Qy     140  HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 199
          |||
Db     121  HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 180

Qy     200  EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 259
          |||
Db     181  EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 240

Qy     260  FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
          |||
Db     241  FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 283
```

# RESULT 3

US-09-855-158-9

```
; Sequence 9, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT:  THEILL, LARS EYDE
; APPLICANT:  YU, GANG
; TITLE OF INVENTION:  METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA, BLYS/AGP-
; TITLE OF INVENTION:  3, AND TACI
; FILE REFERENCE:  A-686A
; CURRENT APPLICATION NUMBER:  US/09/855,158
; CURRENT FILING DATE:  2001-09-11
; PRIOR APPLICATION NUMBER:  US 60/214,591
; PRIOR FILING DATE:  2000-06-27
; PRIOR APPLICATION NUMBER:  US 60/204,039
```

; PRIOR FILING DATE: 2000-05-12  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 283  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-855-158-9

Query Match 90.6%; Score 1488.5; DB 12; Length 283;  
 Best Local Similarity 97.2%; Pred. No. 4.6e-113;  
 Matches 275; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

```

Qy      27 MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGV-----DKTH 79
      |||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAGGGGGDKTH 60

Qy      80 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 139
      |||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 120

Qy     140 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 199
      |||||||||||||||||||||||||||||||||||||||||||||
Db     121 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 180

Qy     200 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 259
      |||||||||||||||||||||||||||||||||||||||||||||
Db     181 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 240

Qy     260 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
      |||||||||||||||||||||||||||||||||||||||||||||
Db     241 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 283
  
```

RESULT 4

US-09-854-864-10  
 ; Sequence 10, Application US/09854864  
 ; Patent No. US20020081296A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THEILL, LARS EYDE  
 ; APPLICANT: YU, GANG  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,  
 BCMA,  
 ; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
 ; FILE REFERENCE: A-686B  
 ; CURRENT APPLICATION NUMBER: US/09/854,864  
 ; CURRENT FILING DATE: 2001-09-11  
 ; PRIOR APPLICATION NUMBER: US 60/204,039  
 ; PRIOR FILING DATE: 2000-05-12  
 ; PRIOR APPLICATION NUMBER: US 60/214,591  
 ; PRIOR FILING DATE: 2000-06-27  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 281  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus

US-09-854-864-10

Query Match 85.1%; Score 1398.5; DB 9; Length 281;  
Best Local Similarity 92.2%; Pred. No. 9.7e-106;  
Matches 261; Conservative 4; Mismatches 9; Indels 9; Gaps 2;

```
Qy      27 MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGV-----DKTH 79
      || || :||||| || ||||: || ||| ||: ||:|||| ||||
Db      1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGSYTG GGGGDKTH 58

Qy      80 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 139
      |||||||||||||||||||||||||||||||||||||||||||||||
Db      59 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 118

Qy     140 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 199
      |||||||||||||||||||||||||||||||||||||||||||||||
Db     119 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 178

Qy     200 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 259
      |||||||||||||||||||||||||||||||||||||||||||||||
Db     179 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 238

Qy     260 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 302
      |||||||||||||||||||||||||||||||||||||||||||||||
Db     239 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 281
```

RESULT 5

US-09-855-158-10

; Sequence 10, Application US/09855158

; Publication No. US20020086018A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,  
BCMA, BLYS/AGP-

; TITLE OF INVENTION: 3, AND TACI

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 281

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-855-158-10

Query Match 85.1%; Score 1398.5; DB 12; Length 281;  
Best Local Similarity 92.2%; Pred. No. 9.7e-106;  
Matches 261; Conservative 4; Mismatches 9; Indels 9; Gaps 2;

```
Qy      27 MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGV-----DKTH 79
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Db 115 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 174

Qy 143 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 202  
 |||

Db 175 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 234

Qy 203 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 262  
 |||

Db 235 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 294

Qy 263 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302  
 |||

Db 295 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 334

RESULT 7

US-10-258-368-6

; Sequence 6, Application US/10258368  
 ; Publication No. US20040013674A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ambrose, Christine  
 ; APPLICANT: Thompson, Jeffrey  
 ; APPLICANT: Schneider, Pascal  
 ; APPLICANT: Rennert, Paul  
 ; TITLE OF INVENTION: Taci As As Anti-Tumor Agent  
 ; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626  
 ; CURRENT APPLICATION NUMBER: US/10/258,368  
 ; CURRENT FILING DATE: 2002-10-21  
 ; PRIOR APPLICATION NUMBER: USSN 60/199,946  
 ; PRIOR FILING DATE: 2000-04-27  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 366  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-258-368-6

Query Match 83.7%; Score 1376; DB 15; Length 366;  
 Best Local Similarity 72.1%; Pred. No. 9.2e-104;  
 Matches 264; Conservative 11; Mismatches 27; Indels 64; Gaps 3;

Qy 1 METDTLLLWVLLLWVPGSTGDVTMLQMA-----GQCSQN 34  
 ||| :

Db 1 METDTLLLWVLLLWVPGSTGDVTMSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEE 60

Qy 35 EYFDSLHACIPCQLRCSSNTP-----P 57  
 :|:| || |: |: |: :

Db 61 QYWDPLLGTCSCKTICNHQSQRTCAAFCRSLSCRKEQGKFYDHLRLDCISCASICGQHP 120

Qy 58 LTCQRYCNASVTNSVK-GVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 116  
 | :| : :| |||

Db 121 KQCA YFCENKL RSPVNL PVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 180

Qy 117 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 176  
 |||

Db 181 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 240



Qy 177 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 236  
 |||||  
 Db 241 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 300  
 Qy 237 ESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 296  
 |||||  
 Db 301 ESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 360  
 Qy 297 SLSPGK 302  
 |||||  
 Db 361 SLSPGK 366

RESULT 8

US-10-411-037-50

; Sequence 50, Application US/10411037

; Publication No. US20040043446A1

; GENERAL INFORMATION:

; APPLICANT: Neose Technologies, Inc.

; APPLICANT: DeFrees, Shawn

; APPLICANT: Zopf, David

; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David

; APPLICANT: Chen, Xi

; APPLICANT: Bowe, Caryn

; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA

; TITLE OF INVENTION: GALACTOSIDASE A

; FILE REFERENCE: 040853-01-5082

; CURRENT APPLICATION NUMBER: US/10/411,037

; CURRENT FILING DATE: 2003-04-09

; PRIOR APPLICATION NUMBER: US 60/328,523

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/344,692

; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/387,292

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: US 60/391,777

; PRIOR FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: US 60/396,594

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/404,249

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 60/407,527

; PRIOR FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 50

; LENGTH: 320

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-411-037-50

Query Match 82.8%; Score 1361; DB 12; Length 320;

Best Local Similarity 82.2%; Pred. No. 1.3e-102;

Matches 263; Conservative 5; Mismatches 34; Indels 18; Gaps 3;

QY 1 METDTLLLWVLLLWVPGSTGDVTM--LQMAQ-----CSQNEYFDSLLHACIPCQL-- 49  
 ||||| : | | | : | |  
 Db 1 METDTLLLWVLLLWVPGSTGDVRRGPRSLRGRDAPAPTPCVPAECFDLLVRHCVACGLLR 60

QY 50 -----RCSSNTPPLTCQRYCNASVTNSVKGVDKTHTCPPCPAPPELLGGPSVFLFPPKP 102  
 || | : |||||  
 Db 61 TPRPKPAGASSPAPRTALQPQESVGAGAGEAAVDKTHTCPPCPAPPELLGGPSVFLFPPKP 120

QY 103 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 162  
 |||||  
 Db 121 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 180

QY 163 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTLC 222  
 |||||  
 Db 181 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTLC 240

QY 223 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 282  
 |||||  
 Db 241 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV 300

QY 283 MHEALHNHYTQKSLSLSPGK 302  
 |||||  
 Db 301 MHEALHNHYTQKSLSLSPGK 320

RESULT 9

US-10-411-026-50

; Sequence 50, Application US/10411026

; Publication No. US20040063911A1

; GENERAL INFORMATION:

; APPLICANT: Neose Technologies, Inc.

; APPLICANT: DeFrees, Shawn

; APPLICANT: Zopf, David

; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David

; APPLICANT: Chen, Xi

; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE

; TITLE OF INVENTION: METHODS

; FILE REFERENCE: 040853-01-5053

; CURRENT APPLICATION NUMBER: US/10/411,026

; CURRENT FILING DATE: 2003-04-09

; PRIOR APPLICATION NUMBER: US 60/328,523

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/344,692

; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/387,292

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: US 60/391,777

; PRIOR FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: US 60/396,594

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/404,249

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 60/407,527

; PRIOR FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 75  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 50  
 ; LENGTH: 320  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-411-026-50

Query Match 82.8%; Score 1361; DB 12; Length 320;  
 Best Local Similarity 82.2%; Pred. No. 1.3e-102;  
 Matches 263; Conservative 5; Mismatches 34; Indels 18; Gaps 3;

```

Qy      1 METDTLLLWVLLLWVPGSTGDVTM--LQMAQ-----CSQNEYFDSLLHACIPCQL-- 49
      ||||| :|: ||| :|: ||
Db      1 METDTLLLWVLLLWVPGSTGDVRRGPRSLRGRDAPAPTPCVPAPAECDLLVRHCVACGLLR 60

Qy      50 -----RCSSNTPPLTCQRYCNASVTNSVKGVDKHTHTCPPCPAPPELLGGPSVFLFPPKP 102
      || | | : |||||
Db      61 TPRPKPAGASSAPRTALQPQESVGAGAGEAAVDKHTHTCPPCPAPPELLGGPSVFLFPPKP 120

Qy     103 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 162
      |||||
Db     121 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 180

Qy     163 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTLC 222
      |||||
Db     181 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTLC 240

Qy     223 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV 282
      |||||
Db     241 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV 300

Qy     283 MHEALHNHYTQKSLSLSPGK 302
      |||||
Db     301 MHEALHNHYTQKSLSLSPGK 320
  
```

# RESULT 10

US-10-193-616-14

; Sequence 14, Application US/10193616  
 ; Publication No. US20030096355A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Ke  
 ; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
 ; TITLE OF INVENTION: ymkz5, a novel  
 ; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family  
 ; FILE REFERENCE: 01017/35551A  
 ; CURRENT APPLICATION NUMBER: US/10/193,616  
 ; CURRENT FILING DATE: 2002-07-11  
 ; PRIOR APPLICATION NUMBER: US/09/611,989  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/143,137  
 ; PRIOR FILING DATE: 1999-07-07  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 14  
 ; LENGTH: 396





|    |     |   |                     |                    |                           |                        |
|----|-----|---|---------------------|--------------------|---------------------------|------------------------|
| Db | 1   |   |                     | :                  |                           |                        |
|    |     | 1 METDTLLLWVLLLWVPGSTGTSCGNSRVDEGEECDPGIMYLNNDTCCNSDCT-LKEGVQC 59 |                     |                    |                           |                        |
| Qy | 32  | SQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNAS----- 67                      |                     |                    |                           |                        |
| Db | 60  | SDRN-----   | SPCCKNCQFETAQKKCQEA | INATCKGVSYCTGNSSEC | PPPGNAEDDT                | 110                    |
| Qy | 68  | -----VTNSVK----- 73   |                     |                    |                           |                        |
| Db | 111 | VCLDLGKCKDGKCI  | PFCE                | EQQL               | ESCACNETDNSCKVCCRDLS      | GRGCVPYVDAEQKNLFLR 170 |
| Qy | 74  | -----GVDKTHTCPPCPA 86   |                     |                    |                           |                        |
| Db | 171 | KGKPC   | TVGFCDMNGKCE        | KRVQDVIERFWDFIDQLS | INTFGKFLADNRSCDKTHTCPPCPA | 230                    |
| Qy | 87  | PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP       |                     |                    |                           | 146                    |
| Db | 231 | PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP       |                     |                    |                           | 290                    |
| Qy | 147 | REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL      |                     |                    |                           | 206                    |
| Db | 291 | REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL      |                     |                    |                           | 350                    |
| Qy | 207 | PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT      |                     |                    |                           | 266                    |
| Db | 351 | PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT      |                     |                    |                           | 410                    |
| Qy | 267 | VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK                              |                     |                    |                           | 302                    |
| Db | 411 | VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK                              |                     |                    |                           | 446                    |

RESULT 13

US-09-792-200B-6

```

; Sequence 6, Application US/09792200B
; Patent No. US20020042368A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Fanslow, William C.
; APPLICANT: Poindexter, Kurt
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: INTEGRIN ANTAGONISTS
; FILE REFERENCE: 2958-A
; CURRENT APPLICATION NUMBER: US/09/792,200B
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/184,865
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Construct
US-09-792-200B-6

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Query Match 77.0%; Score 1265.5; DB 9; Length 465;  
 Best Local Similarity 56.1%; Pred. No. 1.2e-94;  
 Matches 261; Conservative 11; Mismatches 30; Indels 163; Gaps 7;

```

Qy      1 METDTLLLWVLLLWVPGSTG-----DVTM-----L 25
      ||||||||||||||||
Db      1 METDTLLLWVLLLWVPGSTGTSCGNGMVEQGEECDGCGYSDQCKDECCFDANQPEGRKCKL 60

Qy     26 QMAGQCSQNE-----YFDSLLHACIP----- 46
      : ||| :: | :| | |
Db     61 KPGKQCSQSPQGPCCTAQCAFKSKSEKCRDDSDCAREGICNGFTALCPASDPKPNFTDCNR 120

Qy     47 -----CQLRCSSNTPPLTC----- 60
      | : | | |
Db    121 HTQVCINGQCAGSICEKYGLEECTCASSDGKDDKELCHVCCMKMDPSTCASTGQSVQWSR 180

Qy     61 -----QRYCN-----ASVTNSV-----KGVDK 77
      : ||: | : :: : ||
Db    181 HFSGRITITLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKKAI FSPELYENIAERSCDK 240

Qy     78 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 137
      ||||||||| | |||||||||||||||||||||||||||||||||||
Db    241 THTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 300

Qy    138 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 197
      |||||||||||||||||||||||||||||||||||||||||||||||
Db    301 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 360

Qy    198 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 257
      |||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 420

Qy    258 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302
      |||||||||||||||||||||||||||||||||||
Db    421 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465
  
```

RESULT 14

US-10-622-407-14

; Sequence 14, Application US/10622407

; Publication No. US20040018544A1

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2,  
 A NOVEL

; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

; FILE REFERENCE: 01017/35434B

; CURRENT APPLICATION NUMBER: US/10/622,407

; CURRENT FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: US 09/612,033

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14





Query Match 77.0%; Score 1264.5; DB 15; Length 404;  
 Best Local Similarity 77.7%; Pred. No. 1.2e-94;  
 Matches 244; Conservative 6; Mismatches 19; Indels 45; Gaps 3;

```

Qy      33 QNEYFDSLHACIPC-----QLRCSSNTPPLTCQRYCNASVTN----- 70
      |:::|| || || |          :||  ||  :| :  ||
Db      92 QGKFYDHLRDCISCASICGQHPKQCAYFCENKLRSPVNLPP-ELRRQRSGEVENNSDNS 150

Qy      71 -----SVKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 108
      | |||||||||||||||||||
Db     151 GRYQGLEHRGSEASPALPGLKLSADQVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 210

Qy     109 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 168
      |||||||||||||||||||
Db     211 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 270

Qy     169 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 228
      |||||||||||||||||||
Db     271 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY 330

Qy     229 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALH 288
      |||||||||||||||||||
Db     331 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALH 390

Qy     289 NHYTQKSLSLSPGK 302
      |||||||||||
Db     391 NHYTQKSLSLSPGK 404

```

Search completed: April 19, 2004, 13:25:48  
 Job time : 48.2263 secs

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:17:32 ; Search time 44.7407 Seconds  
(without alignments)  
2129.748 Million cell updates/sec

Title: PCT-US03-05147-3  
Perfect score: 1643  
Sequence: 1 METDTLLLWVLLLWVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaphage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result | Query |       |        |    |    |             |
|--------|-------|-------|--------|----|----|-------------|
| No.    | Score | Match | Length | DB | ID | Description |
| -----  |       |       |        |    |    |             |

|    |       |      |     |    |        |                    |
|----|-------|------|-----|----|--------|--------------------|
| 1  | 1243  | 75.7 | 469 | 4  | Q7Z7P5 | Q7z7p5 homo sapien |
| 2  | 1243  | 75.7 | 470 | 4  | Q7Z5W1 | Q7z5w1 homo sapien |
| 3  | 1239  | 75.4 | 482 | 4  | Q7Z351 | Q7z351 homo sapien |
| 4  | 1237  | 75.3 | 679 | 4  | Q96PQ8 | Q96pq8 homo sapien |
| 5  | 1163  | 70.8 | 354 | 4  | Q86TT2 | Q86tt2 homo sapien |
| 6  | 1159  | 70.5 | 521 | 4  | Q8N4Y9 | Q8n4y9 homo sapien |
| 7  | 1148  | 69.9 | 509 | 4  | Q8NF17 | Q8nf17 homo sapien |
| 8  | 1142  | 69.5 | 473 | 4  | Q8TC63 | Q8tc63 homo sapien |
| 9  | 917.5 | 55.8 | 337 | 6  | Q95M34 | Q95m34 equus cabal |
| 10 | 856   | 52.1 | 470 | 11 | Q7TMK1 | Q7tmk1 mus musculu |
| 11 | 841.5 | 51.2 | 469 | 11 | Q8R3V9 | Q8r3v9 mus musculu |
| 12 | 837.5 | 51.0 | 463 | 11 | Q99LC4 | Q99lc4 mus musculu |
| 13 | 833.5 | 50.7 | 437 | 11 | Q9R1A4 | Q9rla4 mus musculu |
| 14 | 826.5 | 50.3 | 473 | 11 | Q9D8L4 | Q9d8l4 mus musculu |
| 15 | 815.5 | 49.6 | 468 | 11 | Q99L31 | Q99l31 mus musculu |
| 16 | 815.5 | 49.6 | 473 | 11 | Q99L25 | Q99l25 mus musculu |
| 17 | 790.5 | 48.1 | 473 | 11 | Q91Z05 | Q91z05 mus musculu |
| 18 | 790.5 | 48.1 | 474 | 11 | Q8R3H6 | Q8r3h6 mus musculu |
| 19 | 358   | 21.8 | 375 | 4  | Q86TT1 | Q86tt1 homo sapien |
| 20 | 358   | 21.8 | 597 | 4  | Q9BU10 | Q9bul0 homo sapien |
| 21 | 358   | 21.8 | 597 | 4  | Q9BQB8 | Q9bqb8 homo sapien |
| 22 | 358   | 21.8 | 597 | 4  | Q96BB9 | Q96bb9 homo sapien |
| 23 | 349   | 21.2 | 614 | 11 | Q7TMT6 | Q7tmt6 mus musculu |
| 24 | 348   | 21.2 | 588 | 4  | Q8WUX4 | Q8wux4 homo sapien |
| 25 | 348   | 21.2 | 613 | 4  | Q96EY0 | Q96ey0 homo sapien |
| 26 | 348   | 21.2 | 613 | 4  | Q8WUK1 | Q8wuk1 homo sapien |
| 27 | 348   | 21.2 | 614 | 4  | Q96GA6 | Q96ga6 homo sapien |
| 28 | 348   | 21.2 | 618 | 4  | Q96AA6 | Q96aa6 homo sapien |
| 29 | 347   | 21.1 | 613 | 11 | Q8VCX7 | Q8vcx7 mus musculu |
| 30 | 316.5 | 19.3 | 587 | 13 | Q7T0R1 | Q7t0r1 xenopus lae |
| 31 | 280   | 17.0 | 384 | 4  | Q9UP60 | Q9up60 homo sapien |
| 32 | 280   | 17.0 | 493 | 4  | Q8NCL6 | Q8ncl6 homo sapien |
| 33 | 280   | 17.0 | 494 | 4  | Q96K68 | Q96k68 homo sapien |
| 34 | 280   | 17.0 | 496 | 4  | Q96KX8 | Q96kx8 homo sapien |
| 35 | 277   | 16.9 | 496 | 4  | Q96DK0 | Q96dk0 homo sapien |
| 36 | 277   | 16.9 | 499 | 4  | Q8N5K4 | Q8n5k4 homo sapien |
| 37 | 275   | 16.7 | 497 | 4  | Q8WY24 | Q8wy24 homo sapien |
| 38 | 275   | 16.7 | 500 | 4  | Q9BRV0 | Q9brv0 homo sapien |
| 39 | 274   | 16.7 | 684 | 13 | Q90544 | Q90544 ginglymosto |
| 40 | 273.5 | 16.6 | 478 | 4  | Q7Z379 | Q7z379 homo sapien |
| 41 | 273.5 | 16.6 | 492 | 4  | Q7Z374 | Q7z374 homo sapien |
| 42 | 271.5 | 16.5 | 416 | 4  | Q9NPP6 | Q9npp6 homo sapien |
| 43 | 269.5 | 16.4 | 486 | 11 | Q91Z07 | Q91z07 mus musculu |
| 44 | 269.5 | 16.4 | 487 | 11 | Q99KA4 | Q99ka4 mus musculu |
| 45 | 268.5 | 16.3 | 426 | 11 | Q9DCD9 | Q9dcd9 mus musculu |

# ALIGNMENTS

## RESULT 1

Q7Z7P5

ID Q7Z7P5 PRELIMINARY; PRT; 469 AA.

AC Q7Z7P5;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```

DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RA      Strausberg R.;
RL      Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC051328; AAH51328.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE    469 AA;  51395 MW;  C8D5BE12BAAF795C CRC64;

```

[illegible]

Db 456 NHYTOKSLSLSPGK 469

## RESULT 2

07Z5W1

SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Matches 234; Conservative 1; Mismatches 11; Indels 8; Gaps 2;

| : | | | | | | | | | | | | | | | | | | | | |



Qy 229 PSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 288  
 |||  
 Db 409 PSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEGLH 468  
 Qy 289 NHYTQKSLSLSPGK 302  
 |||  
 Db 469 NHYTQKSLSLSPGK 482

RESULT 4

Q96PQ8

ID Q96PQ8 PRELIMINARY; PRT; 679 AA.  
 AC Q96PQ8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Factor VII active site mutant immunoconjugate.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21477448; PubMed=11593034;  
 RA Hu Z., Garen A.;  
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
 RT cells for immunotherapy in mouse models of prostatic cancer.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hu Z., Garen A.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF272774; AAK58686.2; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00047; ig; 2.  
 DR Pfam; PF00089; trypsin; 1.

```

ID      Q86TT2                PRELIMINARY;          PRT;    354 AA.
AC      Q86TT2;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Human full-length cDNA clone CS0DI019YF20 of placenta of Homo sapiens
DE      (Human) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;

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RA      Genoscope;
RL      Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RA      Li W.B., Gruber C., Jessee J., Polayes D.;
RT      "Full-length cDNA libraries and normalization.";
RL      Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BX248278; CAD62606.1; -.
DR      GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00407; IGc1; 3.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Plasmid.
FT      NON_TER              1              1
SQ      SEQUENCE      354 AA;   39125 MW;   23B80BF4D2B87A92 CRC64;

```

|    |     |   |     |
|----|-----|---|-----|
| Qy | 46  | PCQLRC-----SSNTPLPTCQRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPK | 101 |
| Db | 102 | PCP-RCPEPKSCDTPP-PCPR-----CPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPK   | 153 |
| Qy | 102 | PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL  | 161 |
| Db | 154 | PKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVSVL   | 213 |
| Qy | 162 | TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT  | 221 |
| Db | 214 | TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT  | 273 |
| Qy | 222 | CLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS     | 281 |
| Db | 274 | CLVKGFYPSDIAVEWESSGQPENNYNTTPMMLDSDGSFFLYSKLTVDKSRWQQGNIFS    | 333 |
| Qy | 282 | VMHEALHNHYTQKSLSLSPGK   | 302 |
| Db | 334 | VMHEALHNRFQKSLSLSPGK  | 354 |

RESULT 6

```

ID      Q8N4Y9          PRELIMINARY;      PRT;      521 AA.
AC      Q8N4Y9;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Primary B-Cells;
RA      Strausberg R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC033178; AAH33178.1; -.
DR      PIR; A60764; A60764.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 4.
DR      SMART; SM00407; IGc1; 3.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE      521 AA;      57156 MW;      2AC7D22E72D6CAA2 CRC64;

```

|    |     |  |     |
|----|-----|--|-----|
| Qy | 46  | PCQLRC-----SSNTPTPLTCQRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPK | 101 |
| Db | 269 | PCP-RCPEPKSCDTPF-PCPR-----CPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPK    | 320 |
| Qy | 102 | PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL   | 161 |
| Db | 321 | PKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRVSVL    | 380 |
| Qy | 162 | TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT   | 221 |
| Db | 381 | TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT   | 440 |
| Qy | 222 | CLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS    | 281 |
| Db | 441 | CLVKGFIYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFS    | 500 |
| Qy | 282 | VMHEALHNHYTQKSLSLSPGK  | 302 |
| Db | 501 | VMHEALHNRFQKSLSLSPGK   | 521 |

RESULT 7  
Q8NF17

```

OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RA      Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT      "The nucleotide sequence of a long cDNA clone isolated from human
RT      spleen.";
RL      Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AK090464; BAC03445.1; -.
DR      PIR; A45874; A45874.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; ig; 3.
DR      SMART; SM00407; IGc1; 3.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 2.
FT      NON_TER      1      1
SQ      SEQUENCE      509 AA; 56111 MW; 089498D8076E863C CRC64;

```

| Qy | 46  | PCQLRC-----SSNTPLLTQRYCNASVTNSVKGVDKTHTCPPCPAPELLGGPSVFLFPPK | 101 |
|----|-----|--|-----|
| Db | 188 | PCP-RCPEPKSCDTPP-PCPR-----CPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPK  | 239 |
| Qy | 102 | PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL | 161 |
| Db | 240 | PKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRVSVL  | 299 |
| Qy | 162 | TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT | 221 |
| Db | 300 | TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT | 359 |
| Qy | 222 | CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS   | 281 |
| Db | 360 | CLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIF    | 419 |
| Qy | 282 | VMHEALHNHYTQKSLSLSP  | 300 |
| Db | 420 | VMHEALHNRETQKSLSLSP  | 438 |

RESULT 8  
O8TC63

```

ID      Q8TC63          PRELIMINARY;          PRT;    473 AA.
AC      Q8TC63;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI TaxID=9606;

```



OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wagner B.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98383416; PubMed=9717671;  
 RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,  
 RA Leibold W., Radbruch A.;  
 RT "Organization of the equine immunoglobulin heavy chain constant region  
 RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";  
 RL Immunobiology 199:105-119(1998).  
 DR EMBL; AJ300675; CAC44624.1; -.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 55.8%; Score 917.5; DB 6; Length 337;  
 Best Local Similarity 58.7%; Pred. No. 9.6e-79;  
 Matches 172; Conservative 42; Mismatches 54; Indels 25; Gaps 3;

Qy 12 LLWVPGSTGDVTMLQ MAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNS 71  
 : : || || : | ::|| : : | : | : |  
 Db 68 MVTVPAST-----WTSETYICNVVHAASNFKVDKRIEPIPDNHQKVCDS----- 112  
 Qy 72 VKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 131  
 || ||||| ||||| : || ||||| : ||||| ||||| | : | : |||||  
 Db 113 -----KCPKCPAPELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFN 164  
 Qy 132 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 191  
 || : ||||| | : | : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
 Db 165 WYMDGVEVRTATTRPKEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTI 224  
 Qy 192 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTT 249  
 : | || : : ||||| | | ||| : : || : ||||| ||| : | : || : ||||| | | ||  
 Db 225 TKTGRSQEPQVYVLAPHPDELSKSKSVTCLVKDFYPPEINIEWQSNQPELETKYSTT 284  
 Qy 250 PPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302  
 ||||| : ||||| : || : ||||| | : | ||||| ||||| : || : |||||  
 Db 285 QAQQDSGDSYFLYSKLSVDRNRWQQGTTFTCGVMHEALHNHYTQKNVSKNPGK 337

# RESULT 10

Q7TMK1

ID Q7TMK1 PRELIMINARY; PRT; 470 AA.  
 AC Q7TMK1;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Breast tumor;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Breast tumor;  
RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC055910; AAH55910.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Query Match 52.1%; Score 856; DB 11; Length 470;  
Best Local Similarity 61.7%; Pred. No. 1e-72;  
Matches 161; Conservative 37; Mismatches 51; Indels 12; Gaps 4;

|    |     |                                     |                              |                             |     |
|----|-----|-------------------------------------|------------------------------|-----------------------------|-----|
| Qy | 52  | SSNTPPLTCQRYCN----                  | ASVTNSVKGVD----              | KTHTCP--PCPAPELLGGPSVFLFPPK | 101 |
|    |     |                                     |                              |                             |     |
| Db | 212 | SSTWPSQTV--ICNVAHPASKTELIKRIEPRIPK  | STPPGSSCPPGNILGGPSVFIFPPK    | 269                         |     |
| Qy | 102 | PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD  | GEVHNATKPREEQYNSTYRVVSVL     | 161                         |     |
|    |     |                                     |                              |                             |     |
| Db | 270 | PKDALMISLTPKVTCVVVDVSEDDPDVHVSFV    | VDNKEVHTAWTQPREAQYNSTFRVVSAL | 329                         |     |
| Qy | 162 | TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG | QPREPQVYTLPPSRDELTKNQVSLT    | 221                         |     |
|    |     |                                     |                              |                             |     |
| Db | 330 | PIQHQQDWMRGKEFKCKVNKALPAPIERTISKPK  | GRAQTPQVYTIPPPREQMSKKKVS     | 389                         |     |
| Qy | 222 | CLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLD  | SDGSFFLYSKLTVDKSRWQQGNVFC    | 281                         |     |
|    |     |                                     |                              |                             |     |
| Db | 390 | CLVTNFFSEAIISVEWERNGELEQDYKNTPPILD  | SDGTYFLYSKLTVDTD             | 449                         |     |

Qy 282 VMHEALHNHYTQKSLSLSPGK 302  
 |:|||||:|:|:| |  
 Db 450 VVHEALHNHHTQKNLSRSPGK 470

RESULT 11

Q8R3V9

ID Q8R3V9 PRELIMINARY; PRT; 469 AA.  
 AC Q8R3V9;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN IGH-4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC024405; AAH24405.1; -.  
 DR PIR; B45837; B45837.  
 DR MGD; MGI:96446; Igh-4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 51.2%; Score 841.5; DB 11; Length 469;  
 Best Local Similarity 51.4%; Pred. No. 2.5e-71;  
 Matches 164; Conservative 45; Mismatches 71; Indels 39; Gaps 8;

Qy 16 PGSTGDTVMTLQ MAGQCSQNEYF-----DSLHACIPCQLRC----- 51  
 ||| : || || | :| | |:  
 Db 158 PGSAAQTNSMVTLG-CLVKG YFPEPVTVTWNSGSLSSGVHT-FPAVLQSDLYTLSSSVTV 215

Qy 52 -SSNTPPLTCQRYCNASVTNSVKGVDKTH-----CPP--CPAPELLGGPSVFLFPPKPK 103  
 || | | || : | || | | | ||: |||:|||||  
 Db 216 PSSTWPSQTVT--CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV---SSVFIFPPKPK 270

Qy 104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163  
 | | |: ||:|||||:| :|||:|:|:| ||| |:|||||:|:|:| || | :  
 Db 271 DVLTLITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTTPREEQFNSTFRSVSELP 330

Qy 164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223  
 :|||||:|:|:| | ||||| ||:|: ||||:| :::|:|:|:|:  
 Db 331 MHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTCM 390

Qy 224 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVM 283

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      : | : | | | : | | | | | | : | : | : | : | : | | | | : | | | : | : | :
Db      391 ITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVL 450

Qy      284 HEALHNHYTQKSLSLSPGK 302
      | | | | : | : | | | | | | |
Db      451 HEGLHNHHTKSLSHSPGK 469

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RESULT 12

Q99LC4

```

ID      Q99LC4          PRELIMINARY;          PRT;      463 AA.
AC      Q99LC4;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Similar to RIKEN cDNA 1810060009 gene.
GN      IGH-4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RL      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC003435; AAH03435.1; -.
DR      PIR; B45837; B45837.
DR      HSSP; P01842; 7FAB.
DR      MGD; MGI:96446; Igh-4.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 3.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 1.
SQ      SEQUENCE      463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

```

```

Query Match          51.0%; Score 837.5; DB 11; Length 463;
Best Local Similarity 51.1%; Pred. No. 5.8e-71;
Matches 163; Conservative 46; Mismatches 71; Indels 39; Gaps 8;

```

```

Qy      16 PGSTGDVTMLQ MAGQCSQNEYF-----DSL LHACIPQLRC----- 51
      | | | : | | | | | | | : | | | :
Db      152 PGSAAQTNSMVTLG-CLVKG YFPEPVTVTWNSGSLSSGVHT-FPAVLQSDLYTLSSSVTV 209

Qy      52 -SSNTPPLTLCQRYCNASVTNSVKGVDKTH-----CPP--CPAPELLGGPSVFLFPPKPK 103
      | | | | | : | | | | | | | | | | | : | | | : | | | :
Db      210 PSSTWPSETVT--CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV---SSVFIFPPKPK 264

Qy      104 DTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
      | | | : | : | | | | | : | : | : | : | | | | | : | | | :
Db      265 DVL TITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELP I 324

Qy      164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
      : | | | | | | | : | : | : | | | | | | | : | : | : | : | :
Db      325 MHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTCM 384

```



Qy 224 VKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVM 283  
 : |:| || |||: |||| ||| | |:|:| |:| ||| | || |: || |:| |||:  
 Db 385 ITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFIYSKLNQKSNWEAGNTFTCSVL 444

Qy 284 HEALHNHYTQKSLSLSPGK 302  
 || ||||: |:| ||| ||||  
 Db 445 HEGLHNHHTKSLSHSPGK 463

RESULT 13

Q9RIA4

ID Q9RIA4 PRELIMINARY; PRT; 437 AA.  
 AC Q9RIA4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Gamma1 heavy chain of Mab7 (Fragment).  
 GN IGH-4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
 RT antibody (Mab 7, its light and heavy chains) and construction of a  
 RT single chain antibody (scFV).";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF152372; AAD40243.1; -.  
 DR PIR; B45837; B45837.  
 DR PDB; 1CQK; 11-SEP-99.  
 DR PDB; 1I9I; 25-DEC-02.  
 DR PDB; 1KCU; 11-MAY-02.  
 DR MGD; MGI:96446; Igh-4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 437 437  
 SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 50.7%; Score 833.5; DB 11; Length 437;  
 Best Local Similarity 50.8%; Pred. No. 1.3e-70;  
 Matches 162; Conservative 47; Mismatches 71; Indels 39; Gaps 8;

Qy 16 PGSTGDVTMLQ MAGQCSQNEYF-----DSL LHACIP CQLRC----- 51  
 ||| : || || ||| :| |||  
 Db 126 PGSAAQTNSMVTLG-CLVKG YFPEPVTVTWNSGSLSSGVHT-FPAVLQSDLYTLSSSVTV 183

Qy 52 --SSNTPLPTCQRYCNASVTVNSVKGVDKTHT-----CPP--CPAPELLGGPSVFLFPPKPK 103  
 || | | || : | ||| | | ||| |||:|||||

Db 184 PSSTWPSETVT--CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV---SSVFIFPPKPK 238

Qy 104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163  
| | | : | | : | | | | | : | : | | | : | : | | | | | : | | | : |

Db 239 DVLITITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPI 298

Qy 164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223  
: | | | | | | | : | : | : | | | | | | | | | | | : | : | : | : | : |

Db 299 MHQDWLNGKEFKCRVNSAAPPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCM 358

Qy 224 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV 283  
: | : | | | | : | | | | | | | : | : | : | : | : | | | | : | | | : |

Db 359 ITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVL 418

Qy 284 HEALHNHYTQKSLSLSPGK 302  
| | | | | : | : | | | | |

Db 419 HEGLHNHHTTEKNLSHSPGK 437

# RESULT 14

Q9D8L4

ID Q9D8L4 PRELIMINARY; PRT; 473 AA.

AC Q9D8L4;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 1810060009Rik protein.

GN IGH-1 OR 1810060009RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.;"

RL Nature 409:685-690(2001).

DR EMBL; AK007918; BAB25349.1; -.



Query Match 49.6%; Score 815.5; DB 11; Length 468;  
Best Local Similarity 54.8%; Pred. No. 7.3e-69;  
Matches 161; Conservative 43; Mismatches 77; Indels 13; Gaps 5;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 22  | VTMLQ MAGQCSQNEY-FDSL LHA---CIPCQLRCSNTPP---LTCQRYCNASVTNSVKG  | 74  |
| Db | 175 | VTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKK   | 234 |
| Qy | 75  | VD---KTHTCPP--CPAPELLGGPSVFLEFPKPKD TLMISRTPEVTCVVVDVSHEDPEV   | 128 |
| Db | 235 | IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL MISLSPMVT CVVVDVSEDDPDV | 294 |
| Qy | 129 | KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNKKEYCKKVS NKALPAPIE | 188 |
| Db | 295 | QISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKALPAPIE  | 354 |
| Qy | 189 | KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKT  | 248 |
| Db | 355 | RTISKPKGSVRAPQVYVLP PPEEEMTKKQVTLTCMVTD FMPEDIYVEWTNNGKTELNYKN | 414 |
| Qy | 249 | TPPVLDSDSGSFFLYSLKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK     | 302 |
| Db | 415 | TEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVV HEGHLNHHHTTKSF SRTPGK      | 468 |

Search completed: April 19, 2004, 13:22:56  
Job time : 45.7407 secs

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:17:02 ; Search time 12.428 Seconds  
(without alignments)  
1265.305 Million cell updates/sec

Title: PCT-US03-05147-3  
Perfect score: 1643  
Sequence: 1 METDTLLLVVLLLVPGSTG.....MHEALHNHYTQKSLSLSPGK 302

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

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# SUMMARIES

| Result No. | Score  | % Query |        |   | DB ID      | Description        |
|------------|--------|---------|--------|---|------------|--------------------|
|            |        | Match   | Length |   |            |                    |
| 1          | 1243   | 75.7    | 330    | 1 | GC1_HUMAN  | P01857 homo sapien |
| 2          | 1153   | 70.2    | 326    | 1 | GC2_HUMAN  | P01859 homo sapien |
| 3          | 1143.5 | 69.6    | 290    | 1 | GC3_HUMAN  | P01860 homo sapien |
| 4          | 1142   | 69.5    | 327    | 1 | GC4_HUMAN  | P01861 homo sapien |
| 5          | 934.5  | 56.9    | 323    | 1 | GC_RABIT   | P01870 oryctolagus |
| 6          | 903.5  | 55.0    | 329    | 1 | GC2_CAVPO  | P01862 cavia porce |
| 7          | 856    | 52.1    | 329    | 1 | GC3_MOUSE  | P22436 mus musculu |
| 8          | 849    | 51.7    | 333    | 1 | GCB_RAT    | P20761 rattus norv |
| 9          | 845    | 51.4    | 398    | 1 | GC3M_MOUSE | P03987 mus musculu |
| 10         | 827    | 50.3    | 326    | 1 | GC1_RAT    | P20759 rattus norv |
| 11         | 826    | 50.3    | 329    | 1 | GCC_RAT    | P20762 rattus norv |
| 12         | 825.5  | 50.2    | 324    | 1 | GC1_MOUSE  | P01868 mus musculu |
| 13         | 820.5  | 49.9    | 393    | 1 | GC1M_MOUSE | P01869 mus musculu |
| 14         | 819.5  | 49.9    | 330    | 1 | GCAA_MOUSE | P01863 mus musculu |
| 15         | 818.5  | 49.8    | 335    | 1 | GCAB_MOUSE | P01864 mus musculu |
| 16         | 814.5  | 49.6    | 399    | 1 | GCAM_MOUSE | P01865 mus musculu |
| 17         | 796    | 48.4    | 322    | 1 | GCA_RAT    | P20760 rattus norv |

|    |       |      |     |   |            |        |             |
|----|-------|------|-----|---|------------|--------|-------------|
| 18 | 789.5 | 48.1 | 336 | 1 | GCB_MOUSE  | P01866 | mus musculu |
| 19 | 784.5 | 47.7 | 405 | 1 | GCBM_MOUSE | P01867 | mus musculu |
| 20 | 362.5 | 22.1 | 421 | 1 | EPC_MOUSE  | P06336 | mus musculu |
| 21 | 358   | 21.8 | 454 | 1 | MUC_HUMAN  | P01871 | homo sapien |
| 22 | 357   | 21.7 | 455 | 1 | MUC_MOUSE  | P01872 | mus musculu |
| 23 | 356   | 21.7 | 391 | 1 | MUCB_HUMAN | P04220 | homo sapien |
| 24 | 353   | 21.5 | 429 | 1 | EPC_RAT    | P01855 | rattus norv |
| 25 | 352   | 21.4 | 428 | 1 | EPC_HUMAN  | P01854 | homo sapien |
| 26 | 349   | 21.2 | 458 | 1 | MUC_RABIT  | P03988 | oryctolagus |
| 27 | 347   | 21.1 | 476 | 1 | MUCM_MOUSE | P01873 | mus musculu |
| 28 | 339   | 20.6 | 479 | 1 | MUCM_RABIT | P04221 | oryctolagus |
| 29 | 332   | 20.2 | 450 | 1 | MUC_CANFA  | P01874 | canis famil |
| 30 | 332   | 20.2 | 454 | 1 | MUC_MESAU  | P06337 | mesocricetu |
| 31 | 330.5 | 20.1 | 457 | 1 | MUC_SUNMU  | P20768 | suncus muri |
| 32 | 310   | 18.9 | 438 | 1 | HVC2_HETFR | P23085 | heterodontu |
| 33 | 295.5 | 18.0 | 299 | 1 | ALC_RABIT  | P01879 | oryctolagus |
| 34 | 294   | 17.9 | 438 | 1 | HVC3_HETFR | P23087 | heterodontu |
| 35 | 287.5 | 17.5 | 446 | 1 | MUC_CHICK  | P01875 | gallus gall |
| 36 | 287   | 17.5 | 370 | 1 | HVC1_HETFR | P23084 | heterodontu |
| 37 | 286.5 | 17.4 | 184 | 1 | TR17_HUMAN | Q02223 | homo sapien |
| 38 | 285   | 17.3 | 461 | 1 | HVCM_HETFR | P23088 | heterodontu |
| 39 | 284.5 | 17.3 | 353 | 1 | ALC1_GORGO | P20758 | gorilla gor |
| 40 | 283   | 17.2 | 393 | 1 | HVC3_HETFR | P23086 | heterodontu |
| 41 | 280   | 17.0 | 353 | 1 | ALC1_HUMAN | P01876 | homo sapien |
| 42 | 271.5 | 16.5 | 340 | 1 | ALC2_HUMAN | P01877 | homo sapien |
| 43 | 262.5 | 16.0 | 344 | 1 | ALC_MOUSE  | P01878 | mus musculu |
| 44 | 251.5 | 15.3 | 481 | 1 | MUCM ICTPU | P23735 | ictalurus p |
| 45 | 184.5 | 11.2 | 513 | 1 | SHS1_MOUSE | P97797 | m protein-t |

# ALIGNMENTS

## RESULT 1

GCl\_HUMAN

ID GCl\_HUMAN STANDARD; PRT; 330 AA.

AC P01857;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ig gamma-1 chain C region.

GNIGHG1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=82274238; PubMed=6287432;

RA Ellison J.W., Berson B.J., Hood L.E.;

RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";

RL Nucleic Acids Res. 10:4071-4079(1982).

RN [2]

RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).

RX MEDLINE=71064024; PubMed=5489771;

RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,

RA Waxdal M.J., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
 RL Biochemistry 9:3161-3170(1970).  
 RN [3]  
 RP SEQUENCE OF 136-329 (EU).  
 RX MEDLINE=71064025; PubMed=5530842;  
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
 RA Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino  
 RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
 RL Biochemistry 9:3171-3181(1970).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN NIE).  
 RX MEDLINE=77070269; PubMed=826475;  
 RA Ponstingl H., Hilschmann N.;  
 RT "The rule of antibody structure. The primary structure of a  
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The  
 RT chymotryptic peptides of the H-chain, alignment of the tryptic  
 RT peptides and discussion of the complete structure.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
 RN [5]  
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
 RX MEDLINE=83289131; PubMed=6884994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
 RT "Three-dimensional structure determination of antibodies. Primary  
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 RN [6]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
 RT characterization of the protein, the L- and H-chains, the  
 RT cyanogen bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the  
 CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC G1M(3) marker and the G1M(non-1) markers.  
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of  
 CC 35, 116, 198, 269 and 272.  
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues

CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.

CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.

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CC -----

DR EMBL; J00228; AAC82527.1; ALT\_INIT.

DR PIR; A93433; GHHU.

DR PDB; 1FC1; 15-JUL-92.

DR PDB; 1FC2; 15-JUL-92.

DR PDB; 1AJ7; 12-NOV-97.

DR PDB; 1D5B; 09-FEB-00.

DR PDB; 1D5I; 09-FEB-00.

DR PDB; 1D6V; 04-OCT-00.

DR PDB; 1DN2; 17-MAY-00.

DR PDB; 1E4K; 06-JUN-01.

DR PDB; 1FCC; 20-JUL-95.

DR PDB; 1HZH; 12-JUN-02.

DR PDB; 1I7Z; 08-AUG-01.

DR PDB; 1IIS; 16-MAY-01.

DR PDB; 1IIX; 16-MAY-01.

DR PDB; 1L6X; 10-APR-02.

DR PDB; 2RCS; 12-NOV-97.

DR Genew; HGNC:5525; IGHG1.

DR MIM; 147100; -.

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0003823; F:antigen binding; TAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_cl.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00407; IGcl; 2.

DR PROSITE; PS50835; IG\_LIKE; 3.

DR PROSITE; PS00290; IG\_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW 3D-structure.

FT NON\_TER 1 1

FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.

FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330 CH3.

FT DISULFID 27 83

FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFID 144 204

FT DISULFID 250 308

FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .).

FT MOD\_RES 330 330 REMOVED POST-TRANSLATIONALLY.





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                |||
Db      257 PS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALH 316
QY      289 NHYTQKSLSLSPGK 302
                |||
Db      317 NHYTQKSLSLSPGK 330

```

RESULT 2

GC2\_HUMAN

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ID      GC2_HUMAN          STANDARD;          PRT;          326 AA.
AC      P01859;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Ig gamma-2 chain C region.
GN      IGHG2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE OF 2-326 FROM N.A.
RX      MEDLINE=82197621; PubMed=6804948;
RA      Ellison J.W., Hood L.E.;
RT      "Linkage and sequence homology of two human immunoglobulin gamma
RT      heavy chain constant region genes.";
RL      Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN      [2]
RP      SEQUENCE OF 88-115 FROM N.A.
RC      TISSUE=Fetal liver;
RX      MEDLINE=83001943; PubMed=6811139;
RA      Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT      "Structure of human immunoglobulin gamma genes: implications for
RT      evolution of a gene family.";
RL      Cell 29:671-679(1982).
RN      [3]
RP      SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC      TISSUE=Fetal liver;
RX      MEDLINE=84235992; PubMed=6329676;
RA      Krawinkel U., Rabbitts T.H.;
RT      "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT      heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT      genes.";
RL      EMBO J. 1:403-407(1982).
RN      [4]
RP      SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX      MEDLINE=81007873; PubMed=6774012;
RA      Wang A.-C., Tung E., Fudenberg H.H.;
RT      "The primary structure of a human IgG2 heavy chain: genetic,
RT      evolutionary, and functional implications.";
RL      J. Immunol. 125:1048-1054(1980).
RN      [5]
RP      SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX      MEDLINE=80001357; PubMed=113060;
RA      Connell G.E., Parr D.M., Hofmann T.;
RT      "The amino acid sequences of the three heavy chain constant region

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RT domains of a human IgG2 myeloma protein.";  
 RL Can. J. Biochem. 57:758-767(1979).  
 RN [6]  
 RP SEQUENCE OF 238-275 (ZIE).  
 RX MEDLINE=80114419; PubMed=118920;  
 RA Hofmann T., Parr D.M.;  
 RT "A note of the amino acid sequence of residues 381-391 of human  
 RT immunoglobulins gamma chains.";  
 RL Mol. Immunol. 16:923-925(1979).  
 RN [7]  
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
 RA Hofmann T., Parr D.M.;  
 RL Submitted (MAR-1980) to the PIR data bank.  
 RN [8]  
 RP SEQUENCE OF 1-121 (DOT).  
 RX MEDLINE=95255298; PubMed=7737190;  
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
 RT "Characterization of the two unique human anti-flavin monoclonal  
 RT immunoglobulins.";  
 RL Eur. J. Biochem. 228:886-893(1995).  
 RN [9]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=72033500; PubMed=4940472;  
 RA Milstein C., Frangione B.;  
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
 RL Biochem. J. 121:217-225(1971).  
 RN [10]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=69064124; PubMed=5782707;  
 RA Frangione B., Milstein C., Pink J.R.L.;  
 RT "Structural studies of immunoglobulin G.";  
 RL Nature 221:145-148(1969).

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DR EMBL; J00230; AAB59393.1; -.  
 DR PIR; A93906; G2HU.  
 DR HSSP; P01857; 1FC1.  
 DR Genew; HGNC:5526; IGHG2.  
 DR MIM; 147110; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region.

| FT | NON_TER  | 1       | 1         |  |
|----|----------|---------|-----------|--|
| FT | DOMAIN   | 1       | 98        | CH1.                                     |
| FT | DOMAIN   | 99      | 110       | HINGE.                                   |
| FT | DOMAIN   | 111     | 219       | CH2.                                     |
| FT | DOMAIN   | 220     | 326       | CH3.                                     |
| FT | DISULFID | 14      | 14        | INTERCHAIN (WITH A LIGHT CHAIN).         |
| FT | DISULFID | 27      | 83        |  |
| FT | DISULFID | 102     | 102       | INTERCHAIN (WITH A HEAVY CHAIN).         |
| FT | DISULFID | 103     | 103       | INTERCHAIN (WITH A HEAVY CHAIN).         |
| FT | DISULFID | 106     | 106       | INTERCHAIN (WITH A HEAVY CHAIN).         |
| FT | DISULFID | 109     | 109       | INTERCHAIN (WITH A HEAVY CHAIN).         |
| FT | DISULFID | 140     | 200       |  |
| FT | DISULFID | 246     | 304       |  |
| FT | SITE     | 156     | 156       | AT OR NEAR THE COMPLEMENT-BINDING SITE.  |
| FT | MOD_RES  | 326     | 326       | REMOVED POST-TRANSLATIONALLY (PROBABLE). |
| FT | VARIANT  | 60      | 60        | S -> A (IN MYELOMA PROTEINS TIL & ZIE).  |
| FT |          |         |           | /FTid=VAR_003889.                        |
| FT | CONFLICT | 109     | 109       | C -> S (IN REF. 3).                      |
| SO | SEQUENCE | 326 AA; | 35884 MW; | 8310878C6878CF9C CRC64;                  |

|    |     |   |     |
|----|-----|---|-----|
| Qy | 61  | QRY-CNASVTNSVKGVDKT-----HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE   | 113 |
|    |     | :   |     |
| Db | 79  | QTYTCNVDPHKSNTKVDKTVERKKCCVECPKPAPP-VAGPSVFLFPPKPKDTLMISRTPE  | 137 |
| Qy | 114 | VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE  | 173 |
|    |     | :                     :     :           :                     |     |
| Db | 138 | VTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE  | 197 |
| Qy | 174 | YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSPDIA | 233 |
|    |     | :   :   |     |
| Db | 198 | YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSPDIA | 257 |
| Qy | 234 | VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ  | 293 |
|    |     | :   |     |
| Db | 258 | VEWESNGQPENNYKTTPPMLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ | 317 |
| Qy | 294 | KLSLSLSPGK 302  |     |
|    |     |   |     |
| Db | 318 | KLSLSLSPGK 326  |     |

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE (DISEASE PROTEIN WIS).  
 RX MEDLINE=81021548; PubMed=6774747;  
 RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;  
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:  
 RT gamma 3 heavy-chain disease protein Wis.";  
 RL Biochemistry 19:4304-4308(1980).  
 RN [2]  
 RP REVISIONS TO 12-97 (PROTEIN WIS).  
 RX MEDLINE=77118561; PubMed=402363;  
 RA Michaelsen T.E., Frangione B., Franklin E.C.;  
 RT "Primary structure of the 'hinge' region of human IgG3. Probable  
 RT quadruplication of a 15-amino acid residue basic unit.";  
 RL J. Biol. Chem. 252:883-889(1977).  
 RN [3]  
 RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).  
 RX MEDLINE=77021516; PubMed=823945;  
 RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;  
 RT "The amino acid sequence of 'heavy chain disease' protein ZUC.  
 RT Structure of the Fc fragment of immunoglobulin G3.";  
 RL Biochem. Biophys. Res. Commun. 71:907-914(1976).  
 RN [4]  
 RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).  
 RX MEDLINE=82247835; PubMed=6808505;  
 RA Alexander A., Steinmetz M., Barritault D., Frangione B.,  
 RA Franklin E.C., Hood L., Buxbaum J.N.;  
 RT "Gamma Heavy chain disease in man: cDNA sequence supports partial  
 RT gene deletion model.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).  
 CC -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra  
 CC interchain disulfide bond at position 7 in addition to the 11  
 CC normally present in the hinge region.  
 CC -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.  
 CC -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the  
 CC Ref.2.  
 CC -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region  
 CC and all of the CH1 region.  
 CC -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all  
 CC of the CH1 region, and part of the hinge compared with normal  
 CC gamma-3 heavy chains.  
 CC -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form  
 CC or another gamma chain subclass.  
 CC -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four  
 CC times as long as in other gamma chains and contains three  
 CC identical 15-residue segments preceded by a similar 17-residue  
 CC segment (12-28).  
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 CC -----  
 DR EMBL; J00231; AAA52805.1; ALT\_SEQ.

DR HSSP; P01857; 1FC1.  
 DR Genew; HGNC:5527; IGHG3.  
 DR MIM; 147120; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;  
 KW Pyrrolidone carboxylic acid.  
 FT DOMAIN 12 73 HINGE.  
 FT DOMAIN 74 183 CH2.  
 FT DOMAIN 184 289 CH3.  
 FT REPEAT 29 43  
 FT REPEAT 44 58  
 FT REPEAT 59 73  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .).  
 FT DISULFID 7 7 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .).  
 FT MOD\_RES 290 290 REMOVED POST-TRANSLATIONALLY.  
 FT VARIANT 126 127 QV -> EB (IN ZUC).  
 FT /FTid=VAR\_003890.  
 FT VARIANT 134 134 P -> L (IN OMM).  
 FT /FTid=VAR\_003891.  
 FT VARIANT 139 139 F -> Y (IN OMM).  
 FT /FTid=VAR\_003892.  
 FT VARIANT 182 182 T -> A (IN OMM).  
 FT /FTid=VAR\_003893.  
 FT VARIANT 227 227 S -> N (IN OMM).  
 FT /FTid=VAR\_003894.  
 FT VARIANT 227 227 MISSING (IN ZUC).  
 FT /FTid=VAR\_003895.  
 FT VARIANT 279 279 F -> Y (IN OMM).  
 FT /FTid=VAR\_003896.  
 SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 69.6%; Score 1143.5; DB 1; Length 290;  
 Best Local Similarity 75.6%; Pred. No. 3e-83;  
 Matches 220; Conservative 19; Mismatches 37; Indels 15; Gaps 4;

Qy 26 QMAG-QCSQNEYFDSLL-----HACIPCQLRCSSNTPPLTCQRYCNASVTNS----- 71  
 || | |: : | | | | :|| | | ::  
 Db 1 QMQGVNCTVSSELKTP LGDTTHTCPRCPEPKSCDTPP-PCPRCPEPKSCDTPPPCPRCPE 59

Qy 72 VKGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 131  
 | | || ||||| ||||| ||||| ||||| ||||| ||||| :|  
 Db 60 PKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFK 119

Qy 132 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 191  
 |||||:|||||||:|:|:|:|||||||:|:|:|:|||||||  
 Db 120 WYVDGVQVHNAKTKPREQQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 179

Qy 192 SKAKGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP 251  
 || ||||| |||||:|:|:|:|||||||:|:|:|:|||||||  
 Db 180 SKTKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPP 239

Qy 252 VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 302  
 :||||||| |||||:||||||| :|||||||  
 Db 240 MLDSGDSFFLYSKLTVDKSRWQQGNIFSCFSVMHEALHNRYTQKSLSLSPGK 290

#### RESULT 4

##### GC4\_HUMAN

ID GC4\_HUMAN STANDARD; PRT; 327 AA.  
 AC P01861;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma-4 chain C region.  
 GNIGHG4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83157104; PubMed=6299662;  
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;  
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene."  
 RL DNA 1:11-18(1981).  
 RN [2]  
 RP SEQUENCE OF 1-30 AND 81-326.  
 RX MEDLINE=70207560; PubMed=4192699;  
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;  
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the  
 RT constant region of a gamma 4 chain."  
 RL Biochem. J. 117:33-47(1970).

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; K01316; AAB59394.1; ALT\_INIT.

DR PIR; A90933; G4HU.  
 DR PDB; 1ADQ; 16-SEP-98.  
 DR Genew; HGNC:5528; IGHG4.  
 DR MIM; 147130; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 220 CH2.  
 FT DOMAIN 221 327 CH3.  
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 83  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 141 201  
 FT DISULFID 247 305  
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 69.5%; Score 1142; DB 1; Length 327;  
 Best Local Similarity 85.4%; Pred. No. 4.6e-83;  
 Matches 216; Conservative 10; Mismatches 25; Indels 2; Gaps 1;

Qy 52 SSNTPPLTCQRYCNASVTNSVKGVDKTH--TCPPCPAPELLGGPSVFLFPPKPKDTLMIS 109  
 | | || | | | : : || |||| |||||  
 Db 75 SLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMIS 134  
 Qy 110 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 169  
 ||||| ||||| ||||| : ||||| |||||  
 Db 135 RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWL 194  
 Qy 170 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 229  
 ||||| ||| : ||||| : ||||| : |||||  
 Db 195 NGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYP 254  
 Qy 230 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN 289  
 ||||| : ||||| : |||||  
 Db 255 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFCSCVMHEALHN 314  
 Qy 290 HYTQKSLSLSPGK 302  
 ||||| ||  
 Db 315 HYTQKSLSLGLK 327

RESULT 5

GC\_RABIT

ID GC\_RABIT STANDARD; PRT; 323 AA.

AC P01870;



DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma chain C region.  
 OS *Oryctolagus cuniculus* (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; *Oryctolagus*.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84030930; PubMed=6313520;  
 RA Bernstein K.E., Alexander C.B., Mage R.G.;  
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
 RT F-I haplotype.";  
 RL Immunogenetics 18:387-397(1983).  
 RN [2]  
 RP SEQUENCE OF 1-128.  
 RX MEDLINE=76135469; PubMed=1243651;  
 RA Pratt D.M., Mole L.E.;  
 RT "Sequence studies on the constant region of the Fd sections of rabbit  
 RT immunoglobulin G of different allotype.";  
 RL Biochem. J. 151:337-349(1975).  
 RN [3]  
 RP SEQUENCE OF 88-266 FROM N.A.  
 RX MEDLINE=83299917; PubMed=6193512;  
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
 RT heavy chain and identification of two genomic C gamma genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
 RN [4]  
 RP SEQUENCE OF 132-161.  
 RX MEDLINE=70110015; PubMed=5461106;  
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
 RT "Sequence studies of the Fd section of the heavy chain of rabbit  
 RT immunoglobulin G.";  
 RL Biochem. J. 116:249-259(1970).  
 RN [5]  
 RP SEQUENCE OF 129-131 AND 155-322.  
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
 RL (In) Killander J. (eds.);  
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
 RL Stockholm (1967).  
 CC -!- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,  
 CC 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15  
 CC markers and Ref.5 the E15 marker.  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
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 CC -----  
 DR EMBL; M16426; AAA31289.1; -.  
 DR PIR; A91749; GHRB.

Query Match 56.9%; Score 934.5; DB 1; Length 323;  
Best Local Similarity 68.0%; Pred. No. 1.1e-66;  
Matches 174; Conservative 33; Mismatches 40; Indels 9; Gaps 3;

## RESULT 6

## GC2\_CAVPO

ID GC2\_CAVPO STANDARD; PRT; 329 AA.  
AC P01862;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma-2 chain C region.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE OF 1-3.  
RA Trischmann T.M.;  
RL Submitted (APR-1975) to the PIR data bank.  
RN [2]  
RP SEQUENCE OF 4-68.  
RX MEDLINE=71058471; PubMed=5538606;  
RA Birshtein B.K., Hussain Q.Z., Cebra J.J.;  
RT "Structure of heavy chain from strain 13 guinea pig  
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the  
RT half-cystine joining heavy and light chains.";  
RL Biochemistry 10:18-25(1971).  
RN [3]  
RP SEQUENCE OF 69-133 AND 312-329.  
RX MEDLINE=71058486; PubMed=5538616;  
RA Turner K.J., Cebra J.J.;  
RT "Structure of heavy chain from strain 13 guinea pig  
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal  
RT and hinge region cyanogen bromide fragments.";  
RL Biochemistry 10:9-17(1971).  
RN [4]  
RP SEQUENCE OF 134-226.  
RX MEDLINE=75036072; PubMed=4429665;  
RA Tracey D.E., Cebra J.J.;  
RT "Primary structure of the CH2 homology region from guinea pig IgG2  
RT antibodies.";  
RL Biochemistry 13:4796-4803(1974).  
RN [5]  
RP SEQUENCE OF 227-311.  
RX MEDLINE=75036073; PubMed=4609467;  
RA Trischmann T.M., Cebra J.J.;  
RT "Primary structure of the CH3 homology region from guinea pig IgG2  
RT antibodies.";  
RL Biochemistry 13:4804-4811(1974).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71058474; PubMed=4922544;  
RA Oliveira B., Lamm M.E.;  
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";  
RL Biochemistry 10:26-31(1971).  
CC -!- MISCELLANEOUS: This chain was isolated from pooled serum of strain  
CC 13 inbred guinea pigs.  
DR PIR; A94553; G2GP.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_cl.

DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON\_TER 1 1  
 FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 28 79  
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 142 202  
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).  
 FT DISULFID 248 308  
 SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 55.0%; Score 903.5; DB 1; Length 329;  
 Best Local Similarity 65.8%; Pred. No. 3.2e-64;  
 Matches 171; Conservative 27; Mismatches 49; Indels 13; Gaps 2;

Qy 55 TPPLTCQRYCNASVTNSVKGVDKT-----HTCPPCPAPELLGGPSVFLFPPKPK 103  
 | | : : | | : | ||| || | | | | : | | | |  
 Db 70 TVPSSQKATCNVAHPASSTKVDKTVEPIRTPZBPBCTCPKCPPPENLGGPSVFIFPPKPK 129  
 Qy 104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163  
 | | | | | | | | | | | | : : | | : | | | | | : | | | : | | | :  
 Db 130 DTLMISLTPRVTCVVVDVSDPEPEVQFTWFDNKPVGNAETKPRVEQYNTTFRVESVLPI 189  
 Qy 164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223  
 | | | | | | : | | | | | | | | | | | | | | | | | : : | | : | | |  
 Db 190 QHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPSRDELSKSKSVSTCL 249  
 Qy 224 VKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 281  
 : | : | : | | | | | | | | | | : | : | : | | | | | | | | : : | |  
 Db 250 IINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSLKLTVDKSAWDQGT 309  
 Qy 282 VMHEALHNHYTQKSLSLSPG 301  
 | | | | | | | | | | : : | | | |  
 Db 310 VMHEALHNHVTQKAISRSPG 329

RESULT 7

GC3\_MOUSE

ID GC3\_MOUSE STANDARD; PRT; 329 AA.  
 AC P22436;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig gamma-3 chain C region, secreted form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85027161; PubMed=6092053;

RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
 RA Tucker P.W., Blattner F.R.;  
 RT "Structural analysis of the murine IgG3 constant region gene";  
 RL EMBO J. 3:2041-2046(1984).

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DR EMBL; J00451; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; B02156; G3MSC.  
 DR HSSP; P01857; 1FC1.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Transmembrane; Alternative splicing.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 52.1%; Score 856; DB 1; Length 329;  
 Best Local Similarity 61.7%; Pred. No. 1.8e-60;  
 Matches 161; Conservative 37; Mismatches 51; Indels 12; Gaps 4;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 52  | SSNTPPLTCQRYCN-----ASVTNSVKGVD-----KTHTCP--PCPAPELLGGPSVFLFPPK | 101 |
|    |     | :  ::       :     :  |     |
| Db | 71  | SSTWPSQTV--ICNVAHPASKTELIKRIEPRIPKPSTPPGSSCPPGNILGGPSVFIFPPK   | 128 |
| Qy | 102 | PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL   | 161 |
|    |     | :: :        :  :  : :          :        :                      |     |
| Db | 129 | PKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQYNSTFRVVSAL   | 188 |
| Qy | 162 | TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT   | 221 |
|    |     | :     :    :    :       :       : :     :    ::::  :           |     |
| Db | 189 | PIQHQQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPREQMSKKKVSALT | 248 |
| Qy | 222 | CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS     | 281 |
|    |     | :  :      :   :     :    :             : :                     |     |
| Db | 249 | CLVTNFFSEAISVEWERNGELEQDYKNTTPPILDSGTIFYLYSKLTVDTDSDLQGEIFTCS  | 308 |
| Qy | 282 | VMHEALHNHYTQKSLSLSPGK  | 302 |
|    |     | :     : : :  |     |
| Db | 309 | VVHEALHNHHTQKNLSRSPGK  | 329 |

RESULT 8

GCB\_RAT

ID GCB\_RAT STANDARD; PRT; 333 AA.  
 AC P20761;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma-2B chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89232738; PubMed=3149946;  
 RA Brueggemann M.;  
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";  
 RL Gene 74:473-482(1988).  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
 DR PIR; PS0018; PS0018.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 6 96 IG-LIKE 1.  
 FT DOMAIN 124 223 IG-LIKE 2.  
 FT DOMAIN 232 328 IG-LIKE 3.  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 80  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 147 207  
 FT DISULFID 253 311  
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 51.7%; Score 849; DB 1; Length 333;  
 Best Local Similarity 52.6%; Pred. No. 6.5e-60;  
 Matches 170; Conservative 42; Mismatches 73; Indels 38; Gaps 6;

Qy 16 PGSTGDVTMLQMAGQCSQNEYF-----DSLLHACIPCQLR-----CSS 53  
 || || | : | || | : | : | : |  
 Db 13 PG-CGDTTSSTVTLGCLVKGYFPEPVTVTWNSGALSSDVHT-FPAVLQSGLYTLTSSVTS 70  
 Qy 54 NTPP---LTCQRYCNASVTSVKGVDKTH-----TCPPCPAPELLGGPSVFLFP 99  
 :| | :|| || | |::: || || |||||:|  
 Db 71 STWPSQTVTCNVAHPASSTKVDKVERNRGGIGHKCPTCPTCHKCPVPELLGGPSVFIFP 130  
 Qy 100 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 159  
 |||| |:|: :||||||| |:|:|:|:|:| ||| |:|:|||||||:|

Db 131 PKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFWNNVEVHTAQTQPREEQYNSTFRVVS 190

QY 160 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS 219  
| : ||||:||||:||||:||||||| || |:|||| : | ::||: ||

Db 191 ALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPKGLVRKPKQVYVMGPPTEQLTEQTVS 250

QY 220 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 279  
|||| || |:| ||| ||| | ||| | ||:|||||:|||| |:||| |

Db 251 LTCLTSGLPNDIGVEWTSNGHIEKNYKNTPEVMDSDGSFFMYSKLNVRSRWDSRAPFV 310

QY 280 CSVMHEALHNHYTQKSLSLSPGK 302  
|||:| ||||: :||:| |||

Db 311 CSVVHEGLHNHHVEKSI SRPPGK 333

# RESULT 9

## GC3M\_MOUSE

ID GC3M\_MOUSE STANDARD; PRT; 398 AA.

AC P03987;

DT 23-OCT-1986 (Rel. 02, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-3 chain C region, membrane-bound form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85027161; PubMed=6092053;

RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

RA Tucker P.W., Blattner F.R.;

RT "Structural analysis of the murine IgG3 constant region gene.";

RL EMBO J. 3:2041-2046(1984).

RN [2]

RP SEQUENCE OF 328-398 FROM N.A.

RX MEDLINE=84041483; PubMed=6314258;

RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,

RA Wall R.;

RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene

RT segment.";

RL Nucleic Acids Res. 11:6775-6785(1983).

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CC -----

DR EMBL; J00451; AAB59655.1; -.

DR EMBL; V01526; CAA24767.1; ALT\_SEQ.

DR PIR; A02156; G3MSM.

DR HSSP; P01857; 1FC1.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_cl.

DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Transmembrane; Alternative splicing.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 FT TRANSMEM 346 362 POTENTIAL.  
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).  
 FT CONFLICT 333 333 E -> G (IN REF. 2).  
 FT CONFLICT 342 342 E -> Q (IN REF. 2).  
 FT CONFLICT 388 388 P -> F (IN REF. 2).  
 SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 51.4%; Score 845; DB 1; Length 398;  
 Best Local Similarity 61.4%; Pred. No. 1.7e-59;  
 Matches 159; Conservative 37; Mismatches 51; Indels 12; Gaps 4;

Qy 52 SSNTPLTCQRYCN----ASVTSNVKGV-----KTHTCP--PCPAPELLGGPSVFLFPPK 101  
 || | | || || | :| :: | | | || :|||||:||||  
 Db 71 SSTWPSQTV--ICNVAHPASKTELIKRIEPRIPKPSPPGSSCPPGNILGGPSVFIFPPK 128  
 Qy 102 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 161  
 ||| |||| | |:||||||| :||:| :|:| | | | |:| | ||||:|||| |  
 Db 129 PKDALMISLTPEVTCVVVDVSEDDPDVHVSFVVDNKEVHTAWTQPREAQYNSTFRVVSAL 188  
 Qy 162 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 221  
 : ||||: |||:||||:|||||||:|||| | | : : ||||:| | |:::| :|||  
 Db 189 PIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPREQMSKKKVSLT 248  
 Qy 222 CLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS 281  
 ||| | : | :||| ||: | :| |||:|||||:||||||| | || :|:| |  
 Db 249 CLVTNFFSEAISVEWERNGELEQDYKNTTPPILDSDGTIFYLYSKLTVDTDSDLQGEIFTCS 308  
 Qy 282 VMHEALHNHYTQKSLSLSP 300  
 |:|||||||:||||:| |  
 Db 309 VVHEALHNHHTQKNLSRSP 327

# RESULT 10

GC1\_RAT

ID GC1\_RAT STANDARD; PRT; 326 AA.  
 AC P20759;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-1 chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]



RP SEQUENCE FROM N.A.  
 RX MEDLINE=89232738; PubMed=3149946;  
 RA Brueggemann M.;  
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";  
 RL Gene 74:473-482(1988).  
 DR PIR; PS0017; PS0017.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 112 HINGE.  
 FT DOMAIN 113 219 CH2.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 50.3%; Score 827; DB 1; Length 326;  
 Best Local Similarity 58.2%; Pred. No. 3.5e-58;  
 Matches 152; Conservative 42; Mismatches 51; Indels 16; Gaps 4;

QY 52 SSNTPPLTCQRYCNASVTNSVKGVDKT-----HTCPPCPAPELLGG---PSVFLFPPK 101  
 || | | : | || | | : | ||:||||  
 Db 72 SSTWPSQTVT--CNVAHPASSTKVDDKIVPRNCGGDCKPC----ICTGSEVSSVFIFPPK 125  
 QY 102 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 161  
 || | | : ||:|||||||:| :||| | :|:| | ||| | :|:| |||:||||| | | |  
 Db 126 PKDVLITITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEEQFNSTFRSVSEL 185  
 QY 162 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 221  
 :|||||||: :|||:| | :||||||| :|: : | ||| :|:|:|:|:|:|:|  
 Db 186 PILHQDWLNGRTFRCKVTSAAFPSPIEKTISKPEGRTQVPHVYTMSPTEEMTQNEVSIT 245  
 QY 222 CLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS 281  
 |:||||| | | |||: |||: | | | | :|:|:|:|:|:| | | :|:| | | |  
 Db 246 CMVKGFIYPPDIYVEWQMNGQPQENYKNTPTMDTDGSYFLYSLNVKKEKWQQGNFTFTCS 305  
 QY 282 VMHEALHNHYTQKSLSLSPGK 302  
 |:| | |||:|:| | | |  
 Db 306 VLHEGLHNHHTKSLSHSPGK 326

RESULT 11  
 GCC\_RAT

ID GCC RAT STANDARD; PRT; 329 AA.  
AC P20762;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma-2C chain C region.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88166903; PubMed=3127222;  
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;  
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant  
RT region cDNA: extensive homology to mouse gamma 3.";  
RL Eur. J. Immunol. 18:317-319(1988).

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DR EMBL; X07189; CAA30169.1; -.  
DR PIR; S00847; S00847.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SM00407; IGcl; 2.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DOMAIN 1 97 CH1.  
FT DOMAIN 98 113 HINGE.  
FT DOMAIN 114 222 CH2.  
FT DOMAIN 223 329 CH3.  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 82  
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 143 203  
FT DISULFID 249 307  
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 50.3%; Score 826; DB 1; Length 329;  
Best Local Similarity 51.6%; Pred. No. 4.2e-58;  
Matches 165; Conservative 51; Mismatches 70; Indels 34; Gaps 7;

Qy 15 VPGSTGDTVTLQMGQCSQNEYF-----DSLHACIPCQLR-----CSSNT 55  
||| :| | | || | :| | | |||  
Db 12 VPGCSGTSGSLVTLG-CLVKGYFPEPVTWKVNSGALSSGVHT-FPAVLQSGLYTLSSSVT 69

```

ID      GC1_MOUSE          STANDARD;          PRT;          324 AA.
AC      P01868;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Ig gamma-1 chain C region secreted form.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=80045036; PubMed=115593;
RA      Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA      Takahashi N., Mano Y.;
RT      "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT      gamma 1 chain gene.";
RL      Cell 18:559-568(1979).
RN      [2]
RP      SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX      MEDLINE=80202559; PubMed=6769752;
RA      Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA      Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT      "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT      cloned in a bacterial plasmid.";
RL      Gene 9:87-97(1980).
RN      [3]
RP      SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX      MEDLINE=80012837; PubMed=113776;
RA      Rogers J., Clarke P., Salser W.;
RT      "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT      heavy chain.";
RL      Nucleic Acids Res. 6:3305-3321(1979).

```

```

RN      [4]
RP      SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX      MEDLINE=78242288; PubMed=98524;
RA      Adetugbo K.;
RT      "Evolution of immunoglobulin subclasses. Primary structure of a
RT      murine myeloma gammal chain.";
RL      J. Biol. Chem. 253:6068-6075(1978).
RN      [5]
RP      DISULFIDE BONDS (MOPC 21).
RX      MEDLINE=73008889; PubMed=5073237;
RA      Svasti J., Milstein C.;
RT      "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL      Biochem. J. 126:837-850(1972).
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=2;
CC          Name=Secreted;
CC          IsoId=P01868-1; Sequence=Displayed;
CC          Note=May be the major isoform;
CC          Name=Membrane-bound;
CC          IsoId=P01869-1; Sequence=External;
CC      -----
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CC      -----
DR      EMBL; V00793; CAA24172.1; -.
DR      EMBL; V00793; CAA24173.1; -.
DR      EMBL; V00793; CAA24174.1; -.
DR      EMBL; V00793; CAA24175.1; -.
DR      EMBL; V00795; CAA24176.1; -.
DR      PIR; A02159; G1MS.
DR      GlycoSuiteDB; P01868; -.
DR      MGD; MGI:96446; Igh-4.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_cl.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; ig; 2.
DR      SMART; SM00407; IGcl; 2.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW      Alternative splicing.
FT      NON_TER      1      1
FT      DOMAIN      1      97      CH1.
FT      DOMAIN      98      110      HINGE.
FT      DOMAIN      111      217      CH2.
FT      DOMAIN      218      324      CH3.
FT      DISULFID      27      82
FT      DISULFID      102      102      INTERCHAIN (WITH A LIGHT CHAIN).
FT      DISULFID      104      104      INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      107      107      INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID      109      109      INTERCHAIN (WITH A HEAVY CHAIN).

```



RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 323-393 FROM N.A.  
 RX MEDLINE=82197626; PubMed=6804950;  
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;  
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly  
 RT conserved transmembrane sequence and a 28-residue intracellular  
 RT domain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).  
 RN [3]  
 RP SEQUENCE OF 323-366 FROM N.A.  
 RX MEDLINE=82115295; PubMed=6799207;  
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
 RA Eisenberg D., Wall R.;  
 RT "Gene segments encoding transmembrane carboxyl termini of  
 RT immunoglobulin gamma chains.";  
 RL Cell 26:19-27(1981).  
 RN [4]  
 RP SEQUENCE OF 1-44 FROM N.A.  
 RX MEDLINE=82222190; PubMed=6283537;  
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
 RT "Nucleotide sequences of gene segments encoding membrane domains of  
 RT immunoglobulin gamma chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Membrane-bound;  
 CC IsoId=P01869-1; Sequence=Displayed;  
 CC Name=Secreted;  
 CC IsoId=P01868-1; Sequence=External;  
 CC Note=May be the major isoform;  
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 CC -----  
 DR EMBL; V00793; CAA24172.1; -.  
 DR EMBL; V00793; CAA24173.1; -.  
 DR EMBL; V00793; CAA24174.1; -.  
 DR PIR; B02159; G1MSM.  
 DR PDB; 15C8; 23-MAR-99.  
 DR PDB; 1AE6; 18-MAR-98.  
 DR PDB; 1CL7; 12-JAN-00.  
 DR PDB; 1F11; 06-FEB-01.  
 DR PDB; 1F58; 29-DEC-99.  
 DR PDB; 1KC5; 24-JUL-02.  
 DR PDB; 1KCR; 11-MAY-02.  
 DR PDB; 25C8; 09-JUL-99.  
 DR MGD; MGI:96446; Igh-4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 2.



DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma-2A chain C region, A allele.  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81076554; PubMed=6777755;  
 RA Sikorav J.-L., Auffray C., Rougeon F.;  
 RT "Structure of the constant and 3' untranslated regions of the murine  
 RT Balb/c gamma 2a heavy chain messenger RNA.";  
 RL Nucleic Acids Res. 8:3143-3155(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81198976; PubMed=6262729;  
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;  
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene  
 RT and evolution of heavy chain genes: further evidence for intervening  
 RT sequence-mediated domain transfer.";  
 RL Nucleic Acids Res. 9:1365-1381(1981).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81223894; PubMed=6787604;  
 RA Ollo R., Auffray C., Morchamps C., Rougeon F.;  
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes  
 RT suggests that exons can be exchanged between genes in a multigenic  
 RT family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).  
 RN [4]  
 RP MYELOMA PROTEIN MOPC 173.  
 RX MEDLINE=74175517; PubMed=4831970;  
 RA Bourgois A., Fougereau M., Rocca-Serra J.;  
 RT "Determination of the primary structure of a mouse IgG2a  
 RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications  
 RT for the evolution of immunoglobulin structure and function.";  
 RL Eur. J. Biochem. 43:423-435(1974).  
 RN [5]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=73056887; PubMed=4565406;  
 RA de Preval C., Fougereau M.;  
 RT "Determination of the primary structure of a mouse gamma G2a  
 RT immunoglobulin. Identification of the disulfide bridges.";  
 RL Eur. J. Biochem. 30:452-462(1972).  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
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 CC -----  
 DR EMBL; V00798; CAA24178.1; -.  
 DR PIR; A02152; G2MSA.  
 DR PDB; 1E4W; 12-JUL-01.



DR PDB; 1E4X; 12-JUL-01.  
 DR PDB; 1MNU; 06-MAY-99.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 6 98 IG-LIKE 1.  
 FT DOMAIN 121 220 IG-LIKE 2.  
 FT DOMAIN 229 325 IG-LIKE 3.  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT MOD\_RES 330 330 REMOVED POST-TRANSLATIONALLY.  
 SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 49.9%; Score 819.5; DB 1; Length 330;  
 Best Local Similarity 54.8%; Pred. No. 1.4e-57;  
 Matches 161; Conservative 43; Mismatches 77; Indels 13; Gaps 5;

Qy 22 VTMLQ MAGQCSQNEY-FDSLHA---CIPCQLRCSSNTTP---LTCQRYCNASVTNSVKG 74  
 ||: :| | : |::| : : : :| | :|| || | |  
 Db 37 VTILTWN SGLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDDK 96  
 Qy 75 VD----KTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 128  
 :: ||| |||| |||||::||| || |||| :| |||||::||:|  
 Db 97 IEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMLSLSPIVTCVVVDVSEDDPDV 156  
 Qy 129 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 188  
 : :|: ||| |::| | ||| ||| | : |||::|||:|||:| |||||  
 Db 157 QISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLPAPIE 216  
 Qy 189 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 248  
 :||| || | ||| ||| :::| ||:|:| | | || ||| :||: | |||  
 Db 217 RTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKN 276  
 Qy 249 TPPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 302  
 | |||||::|:||| |:| | : | :|||:| |||:| || | :|||  
 Db 277 TEPVLDS DGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330

# RESULT 15

## GCAB\_MOUSE

ID GCAB\_MOUSE STANDARD; PRT; 335 AA.  
 AC P01864;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Ig gamma-2A chain C region secreted form (B allele).

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=82037861; PubMed=6170065;  
 RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;  
 RT "Multiple differences between the nucleic acid sequences of the  
 RT IgG2aa and IgG2ab alleles of the mouse."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=82037777; PubMed=6794027;  
 RA Dognin M.J., Lauwereys M., Strosberg A.D.;  
 RT "Multiple amino acid substitutions between murine gamma 2a heavy  
 RT chain Fc regions of Ig1a and Ig1b allotypic forms."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).  
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Secreted;  
 CC IsoId=P01864-1; Sequence=Displayed;  
 CC Note=Probably the major isoform;  
 CC Name=Membrane-bound;  
 CC IsoId=P01865-1; Sequence=External;  
 CC -!- MISCELLANEOUS: The sequence differs from that of the a allele,  
 CC from BALB/c mice, at 15% of the positions.  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; J00479; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A02153; G2MSAB.  
 DR PDB; 1BOG; 23-MAR-99.  
 DR PDB; 1HH6; 26-JAN-01.  
 DR PDB; 1HH9; 24-JUL-03.  
 DR PDB; 1HI6; 08-FEB-01.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;  
 KW 3D-structure; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 6 98 IG-LIKE 1.  
 FT DOMAIN 126 225 IG-LIKE 2.

FT DOMAIN 234 330 IG-LIKE 3.  
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 49.8%; Score 818.5; DB 1; Length 335;  
Best Local Similarity 50.8%; Pred. No. 1.7e-57;  
Matches 162; Conservative 51; Mismatches 73; Indels 33; Gaps 6;

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Qy      17 GSTGD-----VTMLQMAGQCSQNEY-FDSLLHA---CIPCQLRCSSNTPP 57
          |:|||          ||:  :|  |  :  |:||  :  :  :||| |
Db      17 GTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWP 76

Qy      58 ---LTCQRYCNASVTNSVKGVD-----KTHTC-----PPCPAPELLGGPSVFLFPPKPK 103
          :||  || |  | ::  : |  ||| ||:|||||||:|||| |
Db      77 SQTITCNVAHPASSTKVDKKIEPRVPITQNPCPPHQVRVPPCAAPDLLGGPSVFIFPPKIK 136

Qy     104 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 163
          | |||| :| ||||| ||| :||:| :||:| ||| ||:|  | |||| |||| | :
Db     137 DVLMI SLSPMVT CVVDVSEDDPDVQISW FVN NVEVHTAQTQTHREDYNSTLRVVSALPI 196

Qy     164 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 223
          ||||::|||:||||:|:||||:||||||| :|  | |||| ||| :|:| | : ||||:
Db     197 QHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLP PPAEEMTKKEFSLTCL 256

Qy     224 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV 283
          : || |::|||:| |||: | ||| |  |||||:|:|||| | || |:|:|:|:|:|:|:
Db     257 ITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLRVQKSTWERGSLFACSVV 316

Qy     284 HEALHNHYTQKSLSLSPGK 302
          || |||| | |:| | ||
Db     317 HEVLHNHLTTKTISRSLGK 335
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Search completed: April 19, 2004, 13:21:31  
Job time : 13.428 secs